

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 11:59:50 ; Search time 5661 Seconds
(without alignments)

12809.121 Million cell updates/sec

Title: US-10-757-093-3

Perfect score: 1905
Sequence: latgaattccctacggatt.....ctagttatggataagaattaa 1905

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsb1:
9: gb_gsb2:
9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
C 1	261.2	13.7	921	9 CL486845	CL486845 SAIL_443_- AK041058 Mus muscu_- CV169266 rmbx1_01
C 2	222	11.7	2274	3 AK041058	CD014092 90134967
C 3	208.6	11.0	566	7 CV169265	AY321342 Rattus no
C 4	205.8	10.8	1995	6 CD014092	CR593023 full-length
C 5	188.4	9.9	2473	3 C0593823	CD014093 90135266
C 6	183.2	9.6	1377	3 C0593823	BX745933 BX745933
C 7	183.2	9.6	1853	6 CD014093	CL679241 PRI0125C_-
C 8	180.4	9.5	857	5 C0593823	CL679241 PRI0125C_-
C 9	178.8	9.4	811	9 C1679241	CL679241 PRI0125C_-
C 10	175.4	9.2	908	9 C1679241	CD503076 C0593026
C 11	166.2	8.7	1124	6 CD503076	CL478429 SAIL_28_D
C 12	164.8	8.7	907	9 C1478429	CD503076 C0593026
C 13	158.8	8.3	1138	6 CD503076	CF521212 AGENCOURT
C 14	155.4	8.2	7940	7 CF521212	CR442804 CR442804
C 15	150.6	7.9	689	7 CR442804	CB203472 AGENCOURT
C 16	145.6	7.6	914	6 CB203472	CF255373 mdrn17_c
C 17	141.4	7.4	77	7 CF255373	B0941196 AGENCOURT
C 18	139.2	7.3	906	5 B0941196	CL495417 SAIL_60_A
C 19	139	7.3	957	9 CL495417	BX363460 BX363460
C 20	137.8	7.2	1051	5 CL495417	CD503077 C0593077
C 21	137.4	7.2	1268	6 CD503077	CL474664 SAIL_215
C 22	133.6	7.0	913	9 CL474664	CB559443 AGENCOURT
C 23	131	6.9	857	6 CB559443	CL486844 SAIL_443_-
C 24	130.6	6.9	952	9 CL486844	

ALIGNMENTS

25	129.4	6.8	2095	6 CD014094 90135027
c 26	127	6.7	907	9 CL482753 SAIL_367
c 27	126.6	6.6	624	4 BI445636 dae83605-
c 28	126.4	6.6	963	9 CL461373 SAIL_1146
c 29	126.2	6.6	892	9 CL462844 SAIL_1171
c 30	126	6.6	616	2 BI179118 RCO-HTO61
c 31	126	6.6	900	6 CL489317 AGENCOURT
c 32	125.8	6.6	790	7 CO559438 AGENTCOURT
c 33	124.8	6.6	667	7 CN264045 1'0004243
c 34	123.8	6.5	884	9 CL461909 SAIL_1154
c 35	123.2	6.5	802	5 BU357212 603374094
c 36	122.4	6.4	799	5 BU366987 603585124
c 37	121.6	6.4	1023	5 BX3363459 BX3363459
c 38	121.2	6.4	816	7 CK467358 918649 MA
c 39	121	6.4	752	4 BJ733141 BJ733141
c 40	121	6.4	846	6 CA453907 AGENTCOURT
c 41	120.6	6.3	791	5 BU239971 603322761
c 42	120	6.3	603	1 AL676250 AL676250
c 43	119.4	6.3	725	5 BU315788 603851444
c 44	119.4	6.3	777	4 BG741172 602631852
c 45	119	6.2	639	5 BM97809 UI-H-DIO-

RESULT 1				
DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM
SAIL_443_B06_v2, genomic survey sequence.	CL486845	1	GSS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicots; core eudicots; rosids; euroids; III; Brassicales; Brassicaceae; Arabidopsis; Arabidopsis thaliana (thale cress)
1 (bases 1 to 921)	CL486845.1	GI:45965487		
SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., McELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	REFERENCE	AUTHORS		
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bachwaden,J., Ko,C., Clarke,J.D., Bullis,D., Snell,J., Miguel,T., Hutchinson,D., Kimmerly,B., Mitchell,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.	SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	TITLE		
SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	JOURNAL		
Plant Cell 14 (12), 2985-2994 (2002)	SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	MEDLINE		
22356987	SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	PUBMED		
12468722	SESSIONS,A., BURKE,E., PRESTING,G., AUX,G., MCELVER,J., PATTON,D., BULLIS,D., SNELL,J., MIGUEL,T., HUTCHISON,D., KIMMERLY,B., MITCHEL,T., KATAGIRI,F., GLAZEBROOK,J., LAW,M. and GOFF,S.A.	COMMENT		
Contact: Sessions A	Applied Trait Genetics			
SYNGENTA BIOTECHNOLOGY INC.				
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA				
Email: allen.sessions@syngenta.com				
ABRC Stock Number CS20387; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).				
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.				
Class: TDNA tagged.				
Location/Qualifiers				
1. _921				
/organism="Arabidopsis thaliana"				
/mol_type="genomic DNA"				
/ecotype="Columbia"				
/db_xref="Taxon:3702"				
/clone="SAIL_443_B06_v2"				
/clone_lib="SAIL Collection"				
/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"				
ORIGIN				
Query Match	13.7%			
Best Local Similarity	61.2%			
Pred. No. 1.6e-70;				

Matches	442;	Conservative	0;	Mismatches	273;	Indels	7;	Gaps	1;
PUBLISHED	20493159	REFERENCE	10319636	AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	TITLE	Genome Res. 10 (10), 1617-1630 (2000)	JOURNAL					
PUBLISHED	11042159	REFERENCE	3	AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Sumi,N., Ishii,Y., Nakamura,S., Hayama,M., Niinobe,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,M., Itoh,M., Inoue,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
PUBLISHED	556	REFERENCE	1	AUTHORS	Shibata,K., Carninci,P., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Saitoh,R., Togawa,Y., Itoh,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
PUBLISHED	616	REFERENCE	2	AUTHORS	Shibata,K., Carninci,P., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Saitoh,R., Togawa,Y., Itoh,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
PUBLISHED	1392	REFERENCE	3	AUTHORS	Shibata,K., Carninci,P., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Saitoh,R., Togawa,Y., Itoh,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
PUBLISHED	1333	REFERENCE	4	AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection				
PUBLISHED	1512	REFERENCE	5	AUTHORS	Nature 409, 685-690 (2001)				
PUBLISHED	496	REFERENCE	6	AUTHORS	The RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
PUBLISHED	436	REFERENCE	7	AUTHORS	Nature 420, 563-573 (2002)				
PUBLISHED	376	REFERENCE	8	AUTHORS	Adachi,J., Akizawa,K., Aikimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Horii,P., Imotani,K., Ishii,Y., Itoh,M., Kagaishi,T., Kasukawa,T., Koya,S., Kurihara,C., Matsuura,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,I., Sakazume,N., Samo,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tazawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tagami,M., Tomaru,T., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.				
PUBLISHED	256	REFERENCE	9	AUTHORS	Submitted (16-June-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216)				
PUBLISHED	1692	REFERENCE	10	AUTHORS	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://fantom.gsc.riken.jp/				
PUBLISHED	1633	REFERENCE	11	AUTHORS	COMMENT				
PUBLISHED	1612	REFERENCE	12	AUTHORS	AK041058				
PUBLISHED	1572	REFERENCE	13	AUTHORS	2274 bp mRNA linear HTC 03-APR-2004				
PUBLISHED	1512	REFERENCE	14	AUTHORS	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library clone:A530072005 product:beta-glucuronidase structural, full insert sequence.				
PUBLISHED	1512	REFERENCE	15	AUTHORS	AK041058.1 GI:26088231				
PUBLISHED	1512	REFERENCE	16	AUTHORS	HTC; CAP trapper.				
PUBLISHED	74	REFERENCE	17	AUTHORS	AK041058				
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PUBLISHED	74	REFERENCE	212	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	213	AUTHORS	75 AG				
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PUBLISHED	74	REFERENCE	215	AUTHORS	75 AG				
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PUBLISHED	74	REFERENCE	217	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	218	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	219	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	220	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	221	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	222	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	223	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	224	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	225	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	226	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	227	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	228	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	229	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	230	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	231	AUTHORS	75 AG				
PUBLISHED	74	REFERENCE	232						

/tissue_type="Whole Youth Plant"
 /dev_stages="cultured about 1mon-3mon"
 /clone_lib="cDNA Library of *Salvia miltiorrhiza*"
 /note="Organ: Whole Youth Plant; Vector: pBluescript;
 Site_1: EcoRI; Site_2: Xhol; mRNA isolation used
 PolyAtract(r) mRNA Isolation System (PROMEGA, CAT
 No. Z5200) and pBluescript (-) XR cDNA Library Construction
 Kit (Invitrogen, Cat No 200455.) to construct the cDNA library."

ORIGIN

Query Match 11.0%; Score 208.6; DB 7; Length 566;
 Best Local Similarity 62.6%; Pred. No. 6.4e-54; Mismatches 194; Indels 0; Gaps 0;
 Matches 325; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

Qy 1251 AGATCGGATTAACCTAAACCAAGAGAGGCAATTGTGACTCATGC 1310
 Db 48 AGGGCAGTCACCGGAACTAGCAACGCCATTTAACAGAGCTGAC 107
 Qy 1311 CCGACAAACCATGGCAGTGTGTCATGTCATGGCTATGGCAACAGGCCATCTCA 1370
 Db 108 GCGTGACAAACCAACCCAAAGCGCTGTGATGAGGATATGGCAACGACCGATCCG 167
 Qy 1371 TGAATGAGCTGGAGCTGGAACTCTGGAGGAACTGGCACTGGGCTTACAGTCACCTGAC 1430
 Db 168 TCCCCAAAGTGAGGGAAATTGAGCTGGCACTGGGAAAGGAACTGGGATTCAGTCACCTGAC 227
 Qy 1431 ACTCTGGCCTATACATTGTGAGCTGGCACTGGGAAAGGAACTGGGATTCAGTCACCTGAC 1490
 Db 228 GACCGGTGGATCACCTGGCTATGGTGTGAGCTGGGAAAGGAACTGGGATTCAGTCACCTGAC 287
 Qy 1491 TGAATGAGCTGGAGCTGGAAACGACTCTGGGATTCAGTCACCTGAC 1550
 Db 288 CGATCTCTTGTGCTGTGCTGACCGTAAATTACGGATGATGTCACAGCGCGA 347
 Qy 1551 CCTTGAGGAAAGCAGGAGCTTGAAGAGGAGGCTGATGATGGCAAGAAATTCCA 1610
 Db 348 TTGGAAACGGAGAGAAGTACTGGATAATGGGATTGGGATTCAGTCACCTGAC 407
 Qy 1611 CAGGGGGATCTGCTGAGGAAATGGGCAATACCTGGAGGCTTCACTCTATCT 1670
 Db 408 TCAAGGTTATCATCAGGAAACGGCTGGTGTACCTTAGGGGTCACATGTA 467
 Qy 1671 CGGACTGCTTCAAGGGAGACTCCAAAGTACATGGCATGACCTGAGTT 1730
 Db 468 CACCGACATGTGGAGTGAAGATATCGTGTGCTGGTGTGATGTCACCGCCT 527
 Qy 1731 TATCGCATGTGAGTCAGGGGGAGCATTTGCA 1769
 Db 528 TGTGGCTCACGCCGCGTGTGGTGAACGGPATGGAA 566

ORIGIN

Query Match 10.8%; Score 205.8; DB 6; Length 1995;
 Best Local Similarity 50.1%; Pred. No. 7.7e-53; Mismatches 607; Indels 78; Gaps 4;
 Matches 688; Conservative 0; Mismatches 607; Indels 78; Gaps 4;

Qy 553 ATCACGAGGGAAACCGGACTGCGAGAGATCCAGACATCATCTTACAC 612
 Db 399 ATGCCATGTGATCCAAAGGGTTACTTGTCCAGAACATATTTCACATTTCAAC 458
 Qy 613 TATGCTGTCTGGCCGATCTATCGCTTATTCGTCACCCAGAACATATCCAGGAT 672
 Db 459 TAGCTGACTCGACGGCTGTGACTCTCTGACAGAACCCACCATACATGATGAC 518
 Qy 673 ATTACGGTTACAGTGTGATGGTGAATGGCTGTTAACTACAGGGTGAAGTG 732
 Db 519 ATCACGGTACACCCAGCGTGGAGAACGAGTGGCTGGTGTGAAATACAGATCTGTC 578
 Qy 733 GCGAACGAGACGACCGGGCGATCCAGATCTCAGTGTGATGACAGGATGAGCTT 792
 Db 579 AAGGGAGTAACTGTCTCAAGTGGAGGCGCTTTCGATGAGAAACAAGTCGTG 638
 Qy 793 GCAAAGGCCTGGGGAGCTGGGACTGTGACAAUTCCCTCAGCAAGGTATGG----- 846
 Db 639 GCGAAATGGACTGGGACCCAGGGCAACTTAAGGTCAGCCAGGTGTCAGCCCTGTTGGCCG 698
 Qy 847 -----CAACTGGCGGATATTCCTCTACAACTCCAGTCAGTCACATGTC 891
 Db 699 TACCTGATGAGCAAGCCCTGGCPATCTCTATTCTACATGAGGTTGCACTGTCAG 758
 Qy 892 GGTCTTAGCGCGGATGTTGAGACCTAATGGTGTACAGGCGTGTGACTGTCAG 951
 Db 759 ACGTACTGGGCGCTGTGTCAGTCTCACACATCCCTGGGATGCCACTGTGCT 818
 Qy 952 GTTGGCGGGGACAACTTAAATATGGAAAGCTTGTACTTACGGTTTGGCAA 1011
 Db 819 GTCACCAAGACGCCAGTCTCTCATGAGGAAACTTGTATTCACCGGTGTCACAG 878
 Qy 1012 CATGAGAACACAGCGAGTAGTGCAAGGACATGACCCGCATACATGGTCACGATT 1071
 Db 879 CATGGAGATGGGACATCCGGAGAGGCTCGACTGGCGCTGCTGGAAAGGACTC 938
 Qy 1072 CAACTCATGAAATGGATGGAGGAAATTGGACTCTCAACTCTCTAGGGGA 1131
 Db 939 AACCTGCTGTGCTGGCTGGCCATGCACTGGCTTCCGTTGGCAACCTCTATGAGG 998
 Qy 1132 GAGGCTGATGAAATTGGCAATGGAATGGAAATTGGCTGCTGAGAACACCTGGCTT 1191
 Db 999 GAAGCTGCTGAGATGTGCTACCGCTTGTGCTGAGGATGGCTGCTGAGTGTCCGGCTG 1058
 Qy 1192 GGTCCTGAAATGGCTGTGAGGCTGCTGAGTGTGCTGAGTGTGAGTGTGAGG 1251
 Db 1059 GGCCTGGCT-----GGCG 1073
 Qy 1252 GATGGATTAACGATAACCCAGAGGCCAACAGGGCTGCTGAGCTCATGCC 1311
 Db 1074 CAGTCTTCAACAGTGTCTCTGTCATCACACATGAGGAGAGGAGGGTGCCT 1133
 Qy 1312 CGAGACAAACCATGGCAGGAGTGTGAGTGTGCTATGGCTATGGCAACAGGCCATCTCA 1371

Db	1134	ACGGAGCAGAACCCCCCGGCGGTGATGTTCTGGCCACAGGCCCTCGTCCAC	1193
Oy	1372	GAAGATGGCTCGGAATACTTGAGGCCACTGACCAATTGACTCGTCGAACCTGATCCA	1431
Db	1194	CTAGAACATGCTGCCTGCTGAACTGATGTCATAACCAATCCTTGACCC	1253
Oy	1432	ACTGGCCCTATACATTGCTAACGTGGCACCGCACATATGCTGATGTCATAACCAATCCTTGACCC	1491
Db	1254	TCCGGGCGTGTGACCTT-----GTGAGCACTCTAATCAGCAGCACAGGGCCT	1307
Oy	1492	GATCTGTTGATGTCAGTCAGTCAGTAACTGGTATTCGATGTTCTGATGTTCTGACCC	1551
Db	1308	CCCTATGTTGATGTTGATCTGGTGAACAGCTACTACTCTGTTGATCACAGCTACAGGGCAC	1367
Oy	1552	CCTGAGGAGCAGGGAGCTCTGAAGAAGGAGCTGCATGGATGGCAAGAGAAATCCAC	1611
Db	1368	CTTGAGTGTGATGTCAGTCAGTCAGTCAGGACCCAGCTTGAAGATGAGTCA	1427
Oy	1612	AGCCCGATGTCATGACCGAATATGGTCAGTACCTTGCGGCCCTCACTCTATCTC	1671
Db	1428	AGGCCATTATTCAGGAGGAGTTGGACGAGAACAGATGCAAGGTTTACCGAGATCCA	1487
Oy	1672	GACTGCCTGGAGGAGTTCAGTACAAATGCTGATGAAATGTCAGGTT	1731
Db	1488	CTCTCTGATGTTACTGAGAGTACCGAGAACAGCTGCTGAGTACCGAGTC	1547
Oy	1732	GAT-----CGATGAGTCGAGTGGAGCAGGAGCTTGGACTTGGCCATTCCAG	1785
Db	1548	GATCAAAACAGGAGAAATACCGGATCTGGATTTGCCCATTCTCATG	1607
Oy	1786	ACCAACTGGGATCATCGAGAGCGTAACAAGAGGGTTTACCGGTACCGA	1845
Db	1608	ATGAAAGTCGCCAGGAGAGCTGGGGATAAAGGAGATCTCACTGGCAGAGA	1667
Oy	1846	AAGCCAAAGGCCAGCTATGTTGGGGAGGGAGTGTGACTAGTATGATA	1898
Db	1668	CAACCAAAGTCAGCTTCTTGTGAGAGATACTGGAGATGTC	1720
RESULT 5			
AY321342			
LOCUS	AY21342	2473 bp mRNA linear HTC 16-JUL-2003	
DEFINITION	Rattus norvegicus Ac2-223 mRNA, complete cds.		
ACCESSION	AY321342		
VERSION	AY321342.1		
KEYWORDS	HTC		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE	I (bases 1 to 2473)		
AUTHORS	Xu, C.S., Li, W.Q., Li, Y.C., Wang, L., Wang, S.F., Han, H.P., Chang, C.F., Zhao, L.F., Ma, H., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.		
TITLE	Liver regeneration after PH		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2473)		
AUTHORS	Xu, C.S., Li, W.Q., Li, Y.C., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Choi, L.O., Yuan, J.Y., Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.		
FEATURES	Source	/organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /db_xref="taxon:10116" /note="liver regeneration related protein LRG134"	

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 INTLPPYTLPGTVKTDISMYPKYFVODISEPNTYAGLHSVVLYTTSQPN
 IIVTIVDROVGLVWIMISQSDIRQLERLBDGKIVARGTSNEGQKVPRAHL
 WPYLMIEHPAFLSYUWTMTPESDFYUPLVGTRVATVSKPLINGKPYFOCVN
 KHEDSTRGFDPWLLKQNLNLRWLGANSFRSHYPUSEEVNOLCDRIGVIVDE
 EGIVLULQSGFNGVSLRHLIUMDELVRDKHNPVAMWSVANEVSSLEAGYFKL
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 WYKMTOKPITOSEYCAVADSGGLHEPMPMSRATLLENTHLDBKEKKEYVIGEL
 IWNFADEMTQSPLRTVNGKGIIFQRQKPMARFLRERMRMANETRGJLQINQSP
 VVDDEKEVORHQSICGDAADAKLQHVKVQHVNQDSVIAQAGLICSCYCTRNRHABCLKT
 VPSQDAGACERGRQQLIQAQGWAUTINKACSHFOVROLKHVHANSIAVFKPDPLRS
 CILDISAGSA"

ORIGIN

Query Match Similarity 9.91; Score 188.4; DB 3; Length 2473;
 Best Local Similarity 49.01; Pred. No. 2.7e-47; Mismatches 756; Indels 111; Gaps 8;
 Matches 833; Conservative 0; Mismatches 756; Indels 111; Gaps 8;

Oy	247	CCAGTCGGCCCTCTTACACCACTCTCATCAGCGGAGATTCAGGACATGTCGA	306
Db	413	CCGGTCCCTCCAGCTCTCATGACATCCACAGGAGCTCGAACATCTGCG	472
Oy	307	TGGTTTACTACGCTGAGCTGATGTCCTCAAGGGCTGTCGAGCTCATG	357
Db	473	TGGTGTGATGACGGAGCAGTCGTCCTCACAGGGATGACCGAGCAGG	532
Oy	358	CGATCTCGTGAGGCGAATCCGTCAGGACCTGGCGATCTATGTCACACGG	417
Db	533	AGATGCTGTCAGAACGCGCCATGACTATGAGCTGTCGAGTGTGCGATG	592
Oy	418	CTGTGCGCAGGATGTCGGCGCTATACACCTTGAGCGAGCTGTCGAAATAGTC	477
Db	593	CATGGTGGACATGAGGGGTCACCTCCCTTGAGGTCACATACCAAGCTGTC	652
Oy	478	-----GCCCGGAGGATGTCGAGATTCGTCGAGATGGTCACACAGGAGCTTACCCAT	531
Db	653	CAGAGTCGGCCCTGACCCACCTCCGGTCACCATCACACACTGACCC	712
Oy	532	GAGACTATCCACCTGGAAATCA-----CGACAGGGACCGACTGCG	576
Db	713	TATACCCCTCCACCGGACCATGTCACAGACTGTCCTCCATGATCCAGGT	772
Oy	577	AAGAGAATCAGACCTTCACATGACTTACAGTTCACAGTCTGGCTCGCCGATCTAC	636
Db	773	TACTCTCCAGGACATAGCTGTCGACTCTCACTCTGCGGGTCACCGGTCTG	832
Oy	631	TGGCTTATTCGTCACCCAGACATATCCAGGATATCTGGTTCAGATGTT	696
Db	833	GTCTGTCACCCCTACCACTATGATGATATCTGTCGACCTGTCGTC	892
Oy	697	GTGACAAATGGCTGTTAACCTGAGGTGAGTGCGGACCGAGACGGCGAGTC	756
Db	893	CGGACGCTGACTGTCGACCTGAGCTGACCTGACCATTCGAGTC	952
Oy	757	CAGATCTGAGTCGAGGAGGACTATGTCGAAGGCCCTGGAGCTCAGGT	816
Db	953	GAAGTGTCTCTGATGAGTCGACCTGGCCCTGAGACGGATGAGGT	1012
Oy	817	ACTGTCACCAATTCCCTGAGTCAGCTATGGCACACTGGCGCACATTCACACTC	876
Db	1013	CAACTTGGTCCGGCACCTGGTCGCCTTACCTGATGAGCATCCAGCC	1072
Oy	877	CAGGTCAACATGTCGTCGTCGACCTGAGTCGACCTACAT	924
Db	1073	TACCTGTCACCTGGAGGAGTCAGCTGAGTCGTCGTCGACCTACAT	1132

QY 925 TTGCTTACCGGGCGCGGTACTGTCAAGGTTGCCGGTCACAAATCTTAATAATGGAAG 984
 Db 1133 CTCCTCTGCGGGTCTGACAGTGGCTCACAAGGCAAGTCTCATATAATGGGAAG 1192
 QY 985 CCTTCTACTTACCGGTTTGCACAAACATGAGACAGACAGTAGTGCGAAAGACAT 1044
 Db 1193 CCTTCTACTTACCGGTTTGCACAAACATGAGACAGACAGTAGTGCGAAAGACAT 1252
 QY 1045 GACCCAGGATACATGGTCAAGATTCAAATGAGATGGCAATCTT 1104
 Db 1253 GACTGGCTCTGCTGATAAGGATTCAACCTCTCGTCTCTCGGCAATCTT 1312
 QY 1105 CGGACTTCAACTATCCCTAACCGGAGAGGGTCACTGGATGAGGATTCAGAT 1164
 Db 1313 CGGACTTCAACTATCCCTAACCGGAGAGGGTCACTGGATGAGGATTCAGAT 1372
 QY 1165 GTCGGTGTGAGGAAACCTTCCGGAGGGTCACTGGATGAGGATTCAGAT 1224
 Db 1373 GTCGGTGTGAGGAAACCTTCCGGAGGGTCACTGGATGAGGATTCAGAT 1164
 QY 1225 AGTGGTGTGAGGAAACCTTCCGGAGGGTCACTGGATGAGGATTCAGAT 1372
 Db 1422 -----
 QY 1285 AACGAGGGGATTCGGAGCTATGGCGGAGAACATGGCACTGGATGAGGAT 1344
 Db 1448 CTGAGGGTGTGAGGAGGGTGTGGCGGAGGGAACATGGCACTGGATGAGGAT 1507
 QY 1345 TCTATTGCCAAAGGCGCCGCTCTGATGAGATGGCACTGGATGAGGAT 1284
 Db 1508 TCTGTGCCCCAAATGAGGCTGCTCTGCTGAAACCTGGGGTGTGAGGAT 1404
 QY 1562 -----
 Db 1465 CGGACATATGAGCTGATCGATCTGATCTGTTGAGTGTGAGTGTGAGT 1524
 Db 1610 GTTACAGCTCTGTAACTACCATGCCGTTACCTGGAGGTGAGCTGAGT 1669
 QY 1525 TTCGATGTTTCTCAACAGGAGACCTGGAGAGGAGGGCAGCTTAAAGGAG 1584
 Db 1670 TTATCTGGTATCTGAGTACCGGCTCATCTGGGTGATCTGAGCTACTGGAG 1729
 QY 1585 CTGGATGGATGGCAAGAGAAATCCACAGGCGATGGCTACCGGATATGGCGAT 1644
 Db 1730 TTGAGAAGTGTATAAGTGTACAGAGAACGCAATTTCAGGGAGTATGGAGAC 1789
 QY 1645 ACCCTGGAGGCCTCACTTATCTCGAGACTCTTGTGAGGAGAGTCCAGAAC 1704
 Db 1790 GCGCTCTGGCTCATGGATCCACCTCGATGTGAGGAGAGTCCAGAAC 1849
 QY 1705 ATGTTAGACATGATGACATGGAGTTGAT-----CGCATTTGAGTGTGAGGAG 1758
 Db 1850 CTCTGGAGAATTCATTTGATGAGGAGAACGAAAGAACGAAATGCTGAGGAG 1909
 QY 1759 CATGTTGGAACTTGCCTACGACCACTGGTATCATCCAGTGACGCTAAC 1818
 Db 1910 CTCACTGGAAATTGTGACTTCATGAGAACGAGTACCACTGGAGTAAAC 1969
 QY 1819 AACGAGGGATCTTACCTGACAGAGAACCCAAAGATGGCGAGGAG 1878
 Db 1970 AACGAGGGATCTTACCTGACAGAGAACCCAAAGATGGCGAGGAG 2029
 QY 1879 ACGTGGACTTAGTGTGATA 1898
 Db 2030 AGATACTGGAGGATTCGCAA 2049

ACCESSION ..Cot 25-normalized of Homo sapiens (human).
 CR593823
 VERSION CR593823.1 GI:5047630
 KEYWORDS
 SOURCE HNC; CNSI; cDNA.
 ORGANISM Homo sapiens (human)
 REMARK Unpublished
 CONTACT : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 PARADY Avenue
 REFERENCE 1 (bases 1 to 1377)
 AUTHORS Li, W.B., Gruber,C., Jessee,J and Polayer,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Genoscope
 COMMENT 2 (bases 1 to 1377)
 DIRECT Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de sequencage : BP 191 91016 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cnrs.fr)
 WEB : www.genoscope.cnrs.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BCR V sites of the pINVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 LOCATION/Qualifiers 1. 1377
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clonet=CSD001001W21"
 /tissue_type="B cells" (Ramos cell line) Cot 25-normalized"
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 FEATURES source
 ORIGIN
 Query Match 9 6%; Score 183.2; DB 3; Length 1377;
 Best Local Similarity 51.2%; Pred. No. 9; Be=46; Mismatches 468; Indels 57; Gaps 3;
 Matches 551; Conservative 0; Nucleotides 468;
 QY 829 CCCTCGAGTCAGCTATGGGACCTGGCGCATATCTTACCAACTCAGGTCACATC 888
 Db 145 CGTACCTGATGCAAGAACGCCCTGCGCATATCTTACCAACTCAGGTCACATC 204
 QY 889 GTGGCTCTGGGGATGTAGTGACACCTACATTGTCAGTGACGGGGGTSGTACTGTG 948
 Db 205 CAGACTCTGCGCTGTGTGACTCTGACACATCCCTGGGGATCCGACTGTG 264
 QY 949 AAGTTGCGGGTACACANTCTTAAATAATGGAAAGSCTTCTACTTTACGGTTGGC 1008
 Db 265 GCTGTCACCAAGGCCACTTCCTCATCATGGGAACCTTCTTACCGGTGCAAC 324
 QY 1009 AAACATGAGAACACAGCGTAGTGTGCGAACAGCATGACCCGATACAGTTCGAT 1068
 Db 325 AACATGAGAACACAGCGTAGTGTGCGAACAGCATGACCCGATACAGTTCGAT 1068
 QY 1069 TTCCAACTCTGAAATGAGTGTGGGAAATCTTGGACTCTGACTCTTACGGC 1128
 Db 385 TTCAACCTCTGCTGGCTTGGTGCACCTGCGCATACCTTCGTCACGGCACTCCATGCA 444
 QY 1129 GAGAGGGCTGGATTGCGAGATGAGAAATGTCGTGATGATGAAACACCTGC 1188
 Db 445 GAGGAAGTGTGAGATGTGACCGCTATGGATGTTGGTGTGCGATGTCGGGG 504
 QY 1189 GTGGTGTGAACTATGGCTGTGGGATATGTGAGAGTGTCGTGCGCCAAACATTAAG 1248
 Db 505 GTCGGCTCTGGCCCT-----G 519
 QY 1249 CCGAGATCGGATTAACGATAAACCCAGAGGCGGCAACAGGGGATCTGGAGCTATT 1308
 Db 520 CCCAGTCTTCACACGTTCTCTGCGCATACCATGAGGTGATGAGAGTGGTG 579
 QY 1309 GCCCGAGACAAAACCATGCGGAGTCGTCATGTCGTCATGAGAGTGGTGCGGCACT 1368

RESULT 6

CR593823

LOCUS

DEFINITION

full-length cDNA clone CS001001W21 of B cells (Ramos cell line)

1377 bp mRNA linear HTC 21-TUJ-2004

		reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."	
		ORIGIN	
Db	580 CCTAGGGCACACCAACCCCGGTGATGTTGTCGCGGCCAACGACCTGCTCC 639	Query Match 9, 6%; Score 183.2; DB 6; Length 1853; Best Local Similarity 51.2%; Pred. No. 1.1e-45; Matches 551; Conservative 0; Mismatches 468; Indels 57; Gaps 3;	
Oy	1369 CTTGAAGATGGGCTCGGAATACTTGAGCCACTGACAAATTGACTCTGTCRACTGAT 1428		
Db	640 CACCTAGATCTGCTGCTACTACTGATGAGATGGTGTGAC 6 699		
Oy	1429 CCACATGGCCATTACATTGCTTAAGTCGCACCGGACATATCAGTCGATCGATC 1488		
Db	700 CCTCTGGGCTGTGACCTT-----GTGAGCACTCTAATCTGAGCAGACAGGG 753		
Oy	1489 TCTGATCTGTTGATGTCAGTGCATAATCGTATTTCGGATGGATTCTAACACAGGA 1548		
Db	754 GCTCCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 813		
Oy	1549 GACCTGGAGAACAGGGCACCTCTGAAGAAGGCTGATGGATGCCAACGAAATC 1608		
Db	814 CACCTGGAGTCATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873		
Oy	1609 CACAGGGCATGATGCTCATGACCAATATGGTGAGATACCTTGACGGCTTCACTCTPAC 1668		
Db	874 CAGAAGGCCATTTCTGAGGCGAGTATGGAGGAGAACGATTCAGGGTTTACCGAT 933		
Oy	1669 CTGGACTGCCCCTGGACCGAACAGTCAAGTACAATGTCAGTACATGATCCTACAGTG 1728		
Db	934 CACCTCTGATGTCATCTGACGAGTACCTGAGAAAGTGTGCTGAGCTACATCTCGGT 993		
Oy	1729 TTGTAT-----CGCATTTGAGTGTGATGGCAGGGAGATGTTGGAACTTCCGGATTC 1782		
Db	994 CTGGATCAAACGCGACAAATACGGTGGTGGAGCTTCATGGAAATTCGGCAATTC 1053		
Oy	1783 CAGACCAACTTGGTATCATCGAGTAGAGCTAACAGAAAGGGTTTCCCCGTGAC 1842		
Db	1054 ATGACTGACAGTCACCGACGAGGAGTCTGGGAAATAAAGGGATCTCTCGCGAC 1113		
Oy	1843 CGAAAGSCCAAGGGCGAGCTCATAGTTGGGAGAGTGGTGGACTGTTGATAA 1898		
Db	1114 AGACAAACCAAAAGTGCAGCTCTTGGAGAGAGATCTGGAGATGCCAA 1169		
RESULT 7			
CD014093	CD014093 1853 bp mRNA 1 linear EST 21-OCT-2003		
LOCUS	90135266 Single gene library Homo sapiens cDNA, mRNA sequence.		
DEFINITION			
ACCESSION	CD014093		
VERSION	CD014093.1		
KEYWORDS	EST		
SOURCE			
ORGANISM	Homo sapiens		
	Batrachia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1853)		
TITLE	Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Yong, J. and Stuve, L.L.		
JOURNAL	PCR isolation and cloning of novel splice variant mRNAs from known drug target genes		
COMMENT	Genomics 83 (4), 566-571 (2004)		
PORTER	Incyte Corporation		
TEL	3160 Porter Drive, Palo Alto, CA 94304, USA		
FAX	650 621 8639		
EMAIL	pjin@incyte.com.		
FEATURES	Location/Qualifiers		
Source	1. . 1853 /organism="Homo sapiens" /mol_type="mRNA" /db_xref=taxon:9606 "/clone lib="Single gene library" /notes="Vector: pdrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pdrive Cloning vector and sequenced completely using M13 forward and		

RESULT 8	Bx45933/c	Db	1463 ATGACTGACAGTCACGCCAGGAGCTGGGAATTAAGGGTCACTGGCAG 1522
LOCUS	BX45933	DEFINITION	BX45933 xgc-gastrula xenopus tropicalis cDNA clone Tgas06619 3'
VERSION	BX45933.1	REFERENCE	EST: BX45933
AUTHORS	Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.	TITLE	Xenopus tropicalis (western clawed frog)
JOURNAL	Unpublished (2003)	COMMENT	Xenopus tropicalis (western clawed frog) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Ripoidea; Pipidae; Xenopodinae; Xenopus; Silurana. 1 (bases 1 to 857)
FEATURES	source	CONTACT	Croning MDR Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk
		SEQUENCING PRIMER	T7
		SEQUENCING PRIMER ID:	Tgas06619_glkT7
		THIS SEQUENCE IS FROM A XENOPUS GENE COLLECTION (XGC) LIBRARY	This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
		CDNA WAS OLIGO DT PRIMED FROM SUG OF POLY A+ RNA FROM STAGES 10-13	CDNA was oligo dt primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
		ECORI AT THE 5' END AND NOTI AT THE 3' END	Vector: pCS107; Site_1: EcoRI; Site_2: NotI Host: Escherichia coli K12 - blue.
		LOCATION	Location Qualifiers 1. -857
		ORGANISM	/organism="Xenopus tropicalis"
		MOL TYPE	/mol_type="mRNA"
		CLONE	/db_xref="taxon:8364"
		DEV STAGE	/clone="Tgas06619"
		LAB HOST	/lab_host="Escherichia coli K12-blue"
		NOTE	=Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3', end."
ORIGIN			
QUERY MATCH	9.5%	SCORE	180.4; DB 5; LENGTH 857;
BEST LOCAL SIMILARITY	54.4%	PRED. NO.	6.4e-45;
MATCHES	444;	CONSERVATIVE	0;
		MISMATCHES	321;
		INDELS	51;
		GAPS	2;
FEATURES			
		RESULT 9	
LOCUS	CL67924.1	DEFINITION	CL679241 PRI0125c C10.2 - PRI0125c.BR (811) Mixed stage fomid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
VERSION	CL679241.1	REFERENCE	0 (bases 1 to 811)
KEYWORDS	GS.	AUTHORS	Srinivasan, J., Otto, G.W., Kehlow, U., Geisler, R. and Sommer, R.J.
SOURCE	Pristionchus pacificus	TITLE	AppDB: an AceDB database for the nematode satellite organism Pristionchus pacificus
ORGANISM	Pristionchus pacificus	JOURNAL	Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT	Contact: Sommer, R.J. Evolutionary Biology		
	Max-Planck-Institute for Developmental Biology		
	Spemannstr. 37-39, Tuebingen D-72076, Germany		
	Tel: 0 9770 71601379		
	Fax: 0 9770 7150199		
	Email: ralf.sommer@tuebingen.mpg.de		
	This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.		
	Seq primer: T7		
	Class: fosmid ends.		
	Orientation/Qualifiers		

source	Locus	Definition	Accession	Version
	Organism	Definition	SAIL	GSS
1. -811	/organism="Pristionchus pacificus"	CT463714	SAIL_119_H09_v1	linear genomic clone
/mol_type="genomic DNA"	/strains="California"	SAIL_119_H09_v1	genomic survey sequence.	
/db_xref="Taxon:5126"	/clone_lib="Mixed stage var. California"	CT463714.1	GI:45866619	
/notes="Vector: pEPifos-5 Fosmid vector"				
	ORGANISM	Arabidopsis thaliana (thale cress)		
	REFERENCE	Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta; Rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis; Eukaryota; Viridiplantae;		
	AUTHORS	1 (bases 1 to 508) Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwader,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutchinson,D., Kimmyer,B., Mitzel,T., Katagiri,P., Glazebrook,J., Law,M. and Goff,S.A.		
	TITLE	A high-throughput Arabidopsis reverse genetics system		
	JOURNAL	Plant Cell 14 (12), 2985-2994 (2002)		
	MEDLINE	22356987		
	PUBMED	12468722		
	COMMENT	Contact: Sessions A		
		Applied Trait Genetics		
		Syngenta Biotechnology Inc.		
		3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA		
		Email: allen.sessions@syngenta.com		
		ABRC Stock Number CS805872, T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.		
	FEATURES	Class: TDNA tagged.		
	BOURCE	Location/Qualifiers		
		1. .908		
		/organism="Arabidopsis thaliana"		
		/mol_type="genomic DNA"		
		/ecotype="Columbia"		
		/db_xref="taxon:3702"		
		/clone="SAIL_119_H09_v1"		
		/clone_lib="SAIL Collection"		
		/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"		
	ORIGIN			
	Query	Match	DEFINITION	Locus
	Best	Local Similarity	Score	CT463714
	Matches	Conservative	DB	908 bp
		0;	9	DNA linear
		Mismatches	Length	GSS 31-MAR-2004
		146;	908;	
		Indels	0;	
		Gaps	0;	
			0;	
	Qy	1480	GATCGGATCTGTGTTGATGTCAGTGCAATAATGGATTCTGGATGGTAACTCT	1539
	Db	715	GATACCATCAGCGATCTCTGATGCTCTGCCTAACCGTATTAAGGTGTC	656
	Qy	1540	CAAACGGACACCTTGGAGGACAGGGACGCTCTTGAAGAAGAGCTGATGCGAA	1599
	Db	655	CAAACGGGATTTGGAAAGGCAAGGAAGAGTACTCTGGAAAGAAGACCTTCTGCCTCGCAG	596
	Qy	1600	GAGAAATTCCACAGCCGATGTCATGACGAATATGGTCAGAGTACCCCTGAGCCRT	1659
	Db	595	GAGAACTGATGATCACCGATATCATCACCGAATACGGCGTGGATAGTGTGGCGCTG	536
	Qy	1660	CACTCTATCTCGGACTGCGCTTGGAGGAGGTCAGTACAATGCTGAGATGTAC	1719
	Db	535	CACTCATGATCTCCGACATGTCGGTGAAGAGTATCAGTGCTGGTGTGGATATGAT	476
	Qy	1720	CATCGAGTGTGATGCTGAGTGGATGAGCTGAGGAGGAGCTTCGCGCAT	1779
	Db	475	CACCGCGCTCTGATGCGCTAGCCCGTGTGAGAGTGGAAATTCCCGAT	416
	Qy	1780	TTCCAGGACGACTTGGATCATCGGAGTAGCCTAACCTTACCGTACCGT	1839
		15	TTCCAGGACGACTTGGATCATCGGAGTAGCCTAACCTTACCGTACCGT	155

RESULT 10
CL463714/c

RESULT 10
CL463714/c

Db	355	GACGCCAAGCGAAGTCGGGCTTGTGAGCACAGAGACATA 307	QY	1092 AGCAGATTTTCGGACTTCACACTAACCTTACGGAGAGGTCATTGGATTCCAGA 1151
RESULT	11		Db	253 GGCACACTGGTCGGCACAGCCACTACCCCTTGAGAGGATCCTGCAGATGTTGA 312
CD503076		CDS03076 CDA60-C07_x1d-t SHGC-CDA Gasterosteus aculeatus mRNA sequence.	QY	1152 TCGAAATGAAATGTCGGATGATGAAACACTGCCTGGTGTCAACATGCCTGTAT 1211
LOCUS		DEFINITION CDA60-C07_5', mRNA sequence.	Db	313 CGGCATATGCGATGTTGGATAGAGCTGGCCGGSGCTGG----- 354
ACCESSION		CD503076	QY	1212 GGCCTATCTGAGAGTGGGCCAACACATTAGCCAGATGGATTACGATAAAC 1271
VERSION		EST	Db	355 ----- -CTAAAGAGACTTCGAGTTGGACGCC 385
KEYWORDS		Gasterosteus aculeatus (three spined stickleback)	QY	1272 CCAAGAGGCC --CACAGCAGGGATCTGAGCTCATGCCGAGACAAACATSCC 1129
AUTHORS		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.	Db	386 TCTTAAACCCATGCTGGTGTGTCGAGGAGCTGGTACGTGCTCGGAGAACATCCC 445
TITLE	1 (bases 1 to 114)	Kingley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.	QY	1330 AGTGTGTCATGGTCATGGTCAGCTGGCCATGAGAGATGCTGAGATGCTGCGCA 1389
JOURNAL	Expressed sequence tags from Gasterosteus aculeatus	Unpublished (2003)	Db	446 TGTGTGTCATGGTCAGCTGGTCAGCTGGTGTGTCGAGGAGCTGGTACGTGCTCGTGTGATPAC 505
COMMENT	Contact: Kingley, DM	HMB and Department of Developmental Biology	QY	1390 TACTCGAGCCACTGACCAATTGACTTCTCAACTTGTGCACTCGCCATTACATT 1449
Source	Stanford University School of Medicine	Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA	Db	506 TATTCGAACCTGTATAACATACACAAAGAATGATGATCAAACCCGGCCGTA 1490
TEL:	650 725 5954	Fax: 650 725 7739	QY	1450 GCTAAAGTGTGACCTGACGTCAGCTGATCGATCTGAGATGCTGAGCTT 565
EMAIL:	kingsley@cmgm.stanford.edu	Plate: 60	Db	566 ATCACAGACAG-----TACTATGCCAGGATAAGGGCTCTACTGTGAGCTCATC 619
FEATURES	High quality sequence stop: 782.	Locality,Qualifiers	QY	1510 TCTATAATGGTATTCCGATGGATTCTCAACAGAGACCTTGAGGAAGAGGA 1569
source	1. .1124	/1	Db	620 TCGGTAAACAGTTACTTCTCTGTACCGCCACCGGGAGCTCCATC 679
/organism="Gasterosteus aculeatus"		/mo_type="mRNA"	QY	1570 GCTCTTGAAAGGGACTGTGATGGATGGCAAGAAATTCCACAGGGCATCTC 1629
/strain="Salinas river, CA"		/db_xref="taxon:9293"	Db	680 CAGCTCAAACTCTGAGTGTGAACTGAGTGTGAGGAGTCAGAACATCCAGAG 739
/clone="CDA60-C07"			QY	1630 GAATATGGCGAATACCTTGCGAGGCTTCACTCTCTCGGACTGCTCTGGACGA 1689
/sex="mixed male and female"			Db	740 GAATAGGGGGATGCGCGGGCTACAGGATGATGACCCGGTGTAGTTACTGAC 799
/tissue type="heads and internal organs combined"			QY	1690 GAGTCCAAGTACAATGCTAGCATGTTACCATGAGCTGTTGATGATC 1743
/dev_stage="adult"			Db	800 GAGGACGAGGAGTAGTCCTGCGAGCTACACACACTGTGCTGGACCGAA 1689
/clone lib="SHGC-CDA"			QY	1744 TCGATGGCGGGCGGCGAGCTGTGAACTTCTCGGATTTGACGAGAACCTGGTTCATC 1803
/note="Vector: Lambda ZAP Express/PBK-CMV; Site 1: EcoRI (5' adaptor); Site 2: XbaI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XbaI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of PBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the Lambda ZAP Express vector. In vivo excision was then used to generate individual PBK-CMV phagemid clones for EST sequencing."			Db	860 TACCTCATGGCGAACATCTGAGACTTCTGAGCTTCAGGACCCACAGGATCAG 919
ORIGIN	RESULTS	12	QY	1804 CGACTAGACGGTACANGAGGGTTTACCCGTGACCAAGGCCA 1852
Query Match	8.7%; Score 166.2; DB 6; Length 1124;	CL478429/c	Db	920 CGCTGGGGAAACAAAAAGGGTGTCTAGCAGGCAAGGCCAA 968
Best Local Similarity	52.7%; Pred. No. 2.e-40;	LOCUS	QY	
Matches	500; Conservative 0; Mismatches 388; Indels 61; Gaps 4;	DEFINITION CL478429 SAIL_28_D03.v1 SAIL Collection Arabidopsis thaliana genomic clone	Db	
QY		VERSION CL478429	QY	
Db	912 CGACACCTAACATTGCTACGGGCGCGCTACTGCAAGGTGCGGGTCACATTCT 971	ACCESSION CL478429.1 GI:45946527	Db	
Db	73 CGACGCTACACTCTACCGATGGCAGCCGAGCTTACCAAGTCT 132	REFERENCE Sessions,A., Burie,E., Prating,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bawden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Shell,J., Miguel,T., Hutchison,D., Kimerly,R., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.	QY	
QY	972 ATTAATGGAAGGCGCTTCTACCGGTTGCGAACATGAGAGACAGCAGTACCG 1031	ORGANISM Arabidopsis thaliana (thale cress)	Db	
Db	133 CTCACAAAGAGCCCTCTACTTCACGGATATAACAGGACTCTATATCG 1912	KEYWORDS Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Arabidopsis; Viridiplanae; Streptophyta; Embryophyta; Tracheophyta; roids; eurids II; Brassicales; Brassicaceae; Arabidopsis.	QY	
QY	1032 TCGCAAGGAGTGGCCAGGATACATGGTCCACATTCACTCATGAATGGATGG 1091	AUTHORS A high-throughput Arabidopsis reverse genetics system	Db	
Db	193 AGCGAAAGGCTGGACTGGCCCTCATGGAGAGACTTACTATGGATGGTGG 252	TITLE	QY	

JOURNAL	Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE	22356987
PUBLMED	12468722
COMMENT	Contact: Sessions A Applied Trait Genetics Syngenta Bioresearch Inc. 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com ABRC Stock Number: T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
FEATURES	Class: TDNA tagged. Location/Qualifiers 1. . 907 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /ecotype="Columbia" /db_xref="taxon:3702" /clone="SAIL 28 D03 v1" /note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"
ORIGIN	Query Match 8.7%; Score 164.8; DB 9; Length 907; Best Local Similarity 59.2%; Pred. No. 5.7e-40; Matches 302; Conservative 0; Mismatches 202; Indels 6; Gaps 1; Qy 1125 CCGGAGAGAGTCATGGATTGCCAGTCGAATGGATGTGGATGATGAAACACC 1184 Db 828 CGGGGGGGGGCTTGTGCAATGATATGAAATGATGCGATCGTTGATGAAACTGC 769 Qy 1185 TCCGGTGGCTGAAAC-----ATTGCTGTAGGGGTATGTGAGAGTGGTGGCCACA 1238 Db 768 TCTGTGGCTTAACCTCTTGTGAGGGGACACANGGGAAAGA 709 Qy 1239 AACATTGACGCCAGATCGATTACGATAAACCCAGAGGCCCCAACAGGCGATTCG 1298 Db 708 ACTGTACAGCGAGGGCGTCAACGGGAAACTCACGAAAGGGCACITACAGCGGATTA 649 Qy 1299 TCGAGCTCATGGCGAGACAAACCTGCGCTGTGTCATGTGGCTATGGCCACAGA 1358 Db 648 AGAGCTGATASCGCGTCACAAACACCCAAAGCGTGTGATGGATGGATGCCACGA 589 Qy 1359 GCGCGATCTCATGAGAGATGGCTCGGAATACTTGAGCAGTGGCAATTGACTCG 1418 Db 588 ACCGGATACCCCTCCGGAGGGCGACGGGAAATTGGCGCACTGGGGAGGCAACGG 529 Qy 1419 TCACTTGTCAACTCGCCCTATTACATTCTTAAGTCGGCACGCACTATCGCT 1478 Db 528 TAACCTGACCCGACGGCTCCATCACCTGCCTCAATGTAATGTTGCGAGCTCACAC 469 Qy 1479 GCGATGGATCTGTGATCTGCTGATGCTGATGATTAATCGTATTGCGTGGATTC 1538 Db 468 CCTACATCATCGCGATCTCTTGTATGCTGCTGCTGCTGACCTTATTAAGGGTTGT 409 Qy 1539 TCAAACAGGAGGCTTGGAGGAAGGGCAGGGCACCTCTGAAAGGGAGGTGATGGCA 1598 Db 408 CCAAACGGGATTTGTAGGGAGGAAGGTGACTCGAAANAGACTTCGGCTCGA 349 Qy 1599 AGAGAAATTCCACAGGCGATGTCATGAC 1628 Db 348 GCGAGAACTGCACTCAGCGGATTATCAGTC 319
FEATURES	Source /organism="Gasterosteus aculeatus" /mol_type="mRNA" /strain="Salinas river, CA" /db_xref="S4GC-CDA" /clone="CD460-D07" /sex="mixed male and female" /tissue_type="heads and internal organs combined" /dev_stage="adult" /clone_id="S4GC-CDA" /note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoR1 (5' adaptor); Site 2: XbaI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XbaI site. 5 prime adaptors were used containing an EcoR1 cohesive end. The finished cDNAs were inserted in to the ZAP express vector. The sense orientation was unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the Lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
ORIGIN	Query Match 8.3%; Score 158.8; DB 6; Length 1138; Best Local Similarity 52.8%; Pred. No. 5e-38; Matches 502; Conservative 0; Mismatches 387; Indels 61; Gaps 5; Qy 912 CGCACCTACATTGGCTTACGGCGCTGGRACTGTCAGGTGCGGTCAATCTT 971 Db 73 CGAGCTGTAACCTCTACAGTGGCATCCGGACGGTGTACCGTACAGGACCCAGTC 132 Qy 972 ATAATGTAAGGCTTCTACTTACGGTTGCAACATGAGAACAGAGCTAG 1031 Db 133 CTCAAGAAAGCCCTTCTACTTCAGGAGTAATAAACAGAGACTGATTCG 192 Qy 1032 TCGCAAGGACATGCCAGCATACATGTTACGATTCACACTCATGAATGGATGG 1091 Db 193 AGGCAAGGCGTGTGCTGCGCTCATGAGTCAGGACTTAATTAAGGTTGG 252 Qy 1092 AGCAAATCTTGTGGACTTCACTATCCTACGCGGAGGGTCATGGATTCCAGA 1151 Db 253 GGCAACTGTTCCGGCACGCCACTTCCTATGAGGGAGCTCGAGATG 312 Qy 1152 TCGAAATGGAATGTGGTGTGATGATGAAACACTSCTGGTGTCTAACATGCTGTAT 1211 Db 313 CGGCCATGCGATGTGGTGTGAGCGAGGTGGCGGGGGTGGG----- 354
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus (three spined stickleback)
ORGANISM	Bivalvia; Gastropoda; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
TITLE	Expressed sequence tags from Gasterosteus aculeatus
COMMENT	Unpublished (2003) Contact: Kingsley, DM HMM and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA Tel: 650 725 5954 Fax: 650 725 7739 Email: kingsley@cmgm.stanford.edu Plate: 60 High quality sequence stop: 782. Location/Qualifiers
JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
TITLE	Expressed sequence tags from Gasterosteus aculeatus
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
TITLE	Expressed sequence tags from Gasterosteus aculeatus
COMMENT	Unpublished (2003) Contact: Kingsley, DM HMM and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA Tel: 650 725 5954 Fax: 650 725 7739 Email: kingsley@cmgm.stanford.edu Plate: 60 High quality sequence stop: 782. Location/Qualifiers
JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
TITLE	Expressed sequence tags from Gasterosteus aculeatus
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
AUTHORS	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
TITLE	Expressed sequence tags from Gasterosteus aculeatus
COMMENT	Unpublished (2003) Contact: Kingsley, DM HMM and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA Tel: 650 725 5954 Fax: 650 725 7739 Email: kingsley@cmgm.stanford.edu Plate: 60 High quality sequence stop: 782. Location/Qualifiers
JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163
KEYWORDS	EST;
SOURCE	Gasterosteus aculeatus
ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
REFERENCE	1 (bases 1 to 1118)
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SOURCE	Gasterosteus aculeatus
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JOURNAL	Journal of Molecular Biology
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VERSION	CD503098.1 GI:31433163
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ORGANISM	Actinopterygii; Acanthopterygii; Neopterygii; Teleostei; Neoteleostei; Gasterosteidae; Gasterosteus.
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JOURNAL	Journal of Molecular Biology
COMMENT	Journal of Molecular Biology
VERSION	CD503098.1 GI:31433163

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Db	CFR21612	VERSION	EST
Db	CFR21612.1	EST	Xenopus laevis (African clawed frog)
Db	JOURNAL	Xenopus laevis	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Batrachia; Xenopus;
Db	REFERENCE	1 (bases 1 to 740)	NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Db	AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Db	COMMENT	Unpublished (1997)	Tumor Gene Index
Db	Contact:	Daniela S. Gerhard, Ph.D.	Tissue Procurement : Dr. Igor David
Db	Office of Cancer Genomics	Office of Cancer Genomics	CDNA Library Preparation: Life Technologies, Inc.
Db	National Cancer Institute / NIH	National Cancer Institute / NIH	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Db	Bldg. 31 Rm10A07 Bethesda, MD 20892	Bldg. 31 Rm10A07 Bethesda, MD 20892	DNA sequencing by: Agencourt Bioscience Corporation
Db	Email: cgabs@mail.nih.gov	Email: cgabs@mail.nih.gov	Clone distribution: NCI-CGAP clone distribution information can be
Qy	found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM14121 row: n column: 18 High quality sequence stop: 670. Location/Qualifiers		
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Db	FEATURES		
Db	Source		
Qy	ORIGIN		
Db	Query Match		
Db	Best Local Similarity		
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Db	678	AGTGAATATGGGAGCAGATAACATTCTGGTTCACAGTACCCCCCATGTGTTCACT	737
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Db	738	GAA	740

DEFINITION CR442804 mRNA sequence.

ACCESSION CR442804

VERSION CR442804.1

KEYWORDS EST

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

REFERENCE Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus; Siurana.
1 (bases 1 to 689)

AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.

JOURNAL Unpublished (2004)

COMMENT Contact: Croning MDR
Sanger Institute
Email: trop@sanger.ac.uk
Hinxton, Cambridgeshire, CB10 1SA, UK

XENOPUS TROPICALIS SEQUENCE ID: TTBA080n17.p1xSP6

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.

FEATURES

Source	Location/Qualifiers
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Seq primer: SP6

1. . 689

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'mol_type="mRNA"
'db_xref="taxon:8364"
'clone="TTBA080n17"
'der_stage="tailbud (stage 28-30)"
'lab_host="Escherichia coli DH10B."
'clone_id="XGC-tailbud"
'note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud.
ECORI-NotI cut cDNA was then ligated into pS107 with
ECORI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match 7.9% Score 150.6 DB 7; Length 689;
Best Local Similarity 53.9%; Pred. No. 1.6e-35; Indels 51; Gaps 2;
Matches 392; Conservative 0; Mismatches 284; Gaps 2;

Qy 950 AGTTGGGGGACAAATTCTTATAATGGAAAGCCCTCTACTTACCGGTTTGCA 1009
Db 4 AGTCCTGGGACCAATTCTTCATCGAAGAACATCCTTACCGGTTTGCA 63

Qy 1010 AACATGAGACAGCAGTACCTGGCAAGGGCATGCCACATACATGGTCAGATT 1069
Db 64 AACATGAGACATGATGTCAGAGAACAGACTAGTGGTCACTATTGAAAGGATT 123

Qy 1070 TCCAACTCATGAAATGGAAATTCTTGGACTTCACATATCTTACCGG 1129
Db 124 TTAATCTGGAGTGGCTGGCTGCTACTCCCTCCGACGCCATTATCTTATCGAG 183

Qy 1130 AGAGGGCATGATTGGCAAGTGAATGGATGGCTGCTGATGATGAAACACCTGGG 1189
Db 184 AAGAAATGATGAACTTGTGATAATATGGATGGCTGGTGTGATGATGCCCTGGAG 243

Qy 1190 TTTGTCCTGACACATGCCCTGATGGCGTATCTGAGAGTGGCTGCCACAAACATTAGC 1249
Db 244 TCGTATATA-----ATACC 258

Qy 1250 CAGATGGGATTAACCAAGGGCCACAGCAGGGATTTGTGAGCTATGG 1309

Search completed: March 22, 2005, 18:00:12
Job time : 5670 secs

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Qy 1490 CTGATCTTGTGAGTGGTCAATAATCGGATTGGATGGTATTCAAACGGG 1549
Db 493 CACCTATGTTGATGTTAATTTGTAACAGTACTTTCTTGTATGTCATGCGGGC 552

Qy 1550 ACCTGGAGAACAGAGGCGAGCTCTGAAAGAGGCTGATGGCGAAGAAATTCC 1609
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Qy 1670 TCGGACT 1676
Db 673 CCCATT 679

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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model
Run on: March 22, 2005, 18:23:41 ; Search time 4458 Seconds
(w/o alignments)
5413.357 Million cell updates/sec

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Perfect score: 3354

Sequence: 1 MKFLTGLSLSLAAPSICGP.....RKPKAAAMSLRARWTSIDRN 634

Scoring table: BLOSUM62

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Ygapop 1.0	ygapext 0.5
Fgapop 6.0	fgapext 7.0
Delop 6.0	delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

EST:
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2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gb1:
9: gb_gb2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1223.5	37.4	2095	6 CDD14094	CDD14094 90135027
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4	1168.5	34.8	2274	3 AK041058	AK041058 Mus muscu
5	1045.5	31.9	1853	6 CDD14093	CDD14093 90135265
6	946	28.2	1377	3 CR93823	CR93823 full-length
7	803	23.9	1124	6 CDD503076	CDD503076 CDD503076
8	797.5	23.8	1051	5 BX363460	BX363460 BX363460
9	797	23.8	921	9 CL486845	CL486845 SATL_443_

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 2473)	(bases 1 to 2473)	Unpublished	2	Xu,C.S., Li,W.Q., Li,Y.C., Wang,L., Wang,S.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.P., Zhao,L.F., Ma,H., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.	Liver regeneration after PH									
2															
3															
4															
5															
6															
7															
8															
9															

10	770.5	23.0	1138	6 CD503098	CD503098 CD60-D07	11	728.5	21.7	857	5 BX745933	BX745933 BX745933	12	712.5	21.2	811	9 CIG79241	CIG79241 PR0125C	13	705.5	21.0	906	5 BQ941196	BQ941196 AGENCOURT	14	689	20.5	1055	4 BM557676	BM557676 AGENCOURT	15	683	20.4	877	7 CIR406520	CF406520 G	16	681.5	20.3	767	7 CIR255373	CF255373 mbrn127_c	17	674.5	20.1	740	7 CF521612	CF521612 AGENCOURT	18	671.5	20.0	878	7 CN155220	CN155220 942501 MA	19	671.5	20.0	914	6 CB203472	CB203472 AGENCOURT	20	663	19.7	1063	5 BX401772	BX401772 AGENCOURT	21	656	19.6	1063	5 BQF78153	BQF78153 AGENCOURT	22	649.5	19.4	915	5 CA453907	CA453907 AGENCOURT	23	648.5	19.3	846	6 BU357212	BU357212 603474094	24	647.5	19.3	802	5 CIR264047	CN264047 17006000	25	643	19.2	733	7 BR454056	BR454056 BP454056	26	637	19.0	736	5 BU3239978	BU3239978 60323761	27	633.5	18.9	791	5 CR406520	CR406520 CIR406520	28	630.5	18.8	689	7 CIR42804	CR42804 CR42804	29	622.5	18.6	725	5 BU15788	BU315788 60381444	30	621	18.5	566	7 CIR169266	CV169266 rmax1_01	31	620.5	18.5	900	6 CA489317	CA489317 AGENCOURT	32	609.5	18.2	799	5 BU166987	BU366987 603585124	33	609	18.2	771	4 BG121498	BG121498 602352820	34	605.5	18.1	731	7 CIR105482	CY105482 AGENCOURT	35	601.5	17.9	790	7 C0559438	C0559438 AGENCOURT	36	601	17.9	680	5 CIR36522	CR836522 4061270 B	37	591	17.6	898	5 BU179563	BU179563 GENCOURT	38	590	17.6	962	5 BR084422	BR084422 AGENCOURT	39	587.5	17.5	773	7 CIR748482	CF748482 UI-M-HJU-	40	585.5	17.5	757	4 BI851705	BI851705 60337940	41	583.5	17.4	847	5 BX21253	BX621253 BX21253	42	582	17.4	925	5 BO79162	BO679162 AGENCOURT	43	578.5	17.2	624	4 BI45636	BI45636 dce83e05	44	577.5	17.2	673	6 CBB41568	CBB41568 M15E-2121	45	573	17.1	857	6 CBB59443	CBB59443 AGENCOURT
ALIGNMENTS																																																																																																																																																																																																																							
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Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.P., Zhao,L.F., Ma,H., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.																																																																																																																																																																																																																							
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Direct Submission																																																																																																																																																																																																																							
Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China																																																																																																																																																																																																																							
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QY 585 GlvglgIvalTrpRnpheAlaAspPheGlnThrAsnLeuGlyLeuIleArgValAsp 604
Db 1904 GGAGACTCTCTGAAATTGTCGACTTCATGAGAACAGTCACAGTGGAGACTAAC 1963
QY 605 GlyAlnLysIysGlyValPheThrArgAspArgLysProLyValAlaAlaLysSerLeu 624
Db 1964 GGAACAAAGGCGATCTCAGTCAGCAGAACCCAGATGCGACCTCTTGG 2023
QY 625 ArgAlaArgTrpThrSerLeu 631
Db 2024 CGAGGAGATACTGGAGATT 2044

RESULT 2

CD014094 CD014094 2025 bp mRNA linear EST 21-OCT-2003
LOCUS 9013527 Single gene library Homo sapiens cDNA, mRNA sequence.
DEFINITION CD014094.1 GI:3777623
ACCESSION CD014094
VERSION 1
KEYWORDS EST, Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jin,P., Pu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
Au-Young,J. and Stuve,L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
JOURNAL Genomics 83 (4), 566-571. (2004)
COMMENT Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES

source
1. .2095
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.: 4.21e-129 Length: 2095
Score: 1253.50 Matches: 266
Percent Similarity: 57.51% Conservative: 90
Best Local Similarity: 42.97% Mismatches: 187
Query Match: 37.37% Indels: 77
DB: 6 Gaps: 13

US-10-757-093-4 (1-634) x CD014094 (1-2095)

QY 42 ProGlnArgThrSerSerArgGluLeuValAlaAspGlyLeuTrpLysPheAlaLeu 61
Db 101 CCCCGGAGAGCCCTCGCGGAGTCGAAGGAGCTGACGCCCTTGACCTTC----- 154
QY 62 AlasSerGlyLeuAspAspThr-----AlaGlnProTrpThrAlaPro 75
Db 155 CGCGCGACTCTCGACAACCGAGCCGGAGCTTGAGGGAGCTGGTACCGGGGCC 214
QY 76 LeuProLyS-----LeuGluCyProValProLysSerTyrAlanAspIlePhe 92
Db 215 CTGCGGAGTCAGGCCACCGTGACATSCAGTCAGTCAGTCAGTCAGTCAGC 274
QY 93 IleSerArgGluIleHisAspHisValGlyTrpValTyrTyrGlnArgGluValIleVal 112

Db 275 CAGGACTGGCTCTGGGCATTGGCGCTGGTGGGAGGTGGTGGAGCT 334
QY 113 ProLyGlyTrpSerGlnGlu-----ArgTyrLeuValArgLysGluSerAlaThr 129
Db 335 CGGAGCGATGACCCAGGACCTGCCACAGAGTGGTGTGAGGTTGGCGCAT 394
QY 130 HisHisGlyArgLysLeuValAspAsnArgLysLeuValAlaGluHisValGlyLysTyrThr 149
Db 395 TCTATGCCATGTTGGGAAATGGTCACACCCCTAGAGCTAGGCTAGGCTACCTC 454
QY 150 ProPheGluAlaAspValTrpGluLeuValAlaProGly-----GluLysPheArg 166
Db 455 CCCTTGAGGCGACCTCACACCCGGTCCACCCGGCTAGGCTAGGCGCTCCGGCTCCGA 514
QY 167 LeuThrIleGlyValAsnArgLysLeuValIleProProGlyLysLe----- 185
Db 515 ATCACTATCGCCATCACACACACTCACCCACCCGACGACATCCAA 574
QY 186 -----ThrArgYAsnAlaThrIleGlyArgLysLeuValThrArgLysThr 201
Db 575 TACCTGACTGACACCTCCAAAGTATCCAAAGGTTACTTGGCAGACACTATTGAC 634
QY 202 PhetyrAsnTrpAlaGlyLeuAlaArgSerIlePheLeuIleProProValProGlnGlnHis 221
Db 635 TTTCGAACTTGCGGACTCGCGACCTGAGGCTCTACTCTGTCACGACACCACCTAC 694
QY 222 IleGlnAspIleThrValValThrAspValAspGlyAspArgLysLeuIleAsnTyrGlu 241
Db 695 ATCGATGACATCACCTCACCCACCCGAGCAAGACAGCTGGCTGGATTAACAG 754
QY 242 ValGluValAlaAspGlnThrThrGlyGlnIleSerValLeuAspGluArgly 261
Db 755 ATCTCTGTCAGGGCGTAACTGTTCAAGTTGGAGTGCCTCTTTGAGTCAGAAC 814
QY 262 AlanLeuValAlaLysAlaSerGlyAlaGlnAlaGlyThrValThrValProSerValLeu 281
Db 815 AAAGCTGGGGCATGGACTGGGACCCGGCCACCTAAAGCTGGGGTCACCTC 874
QY 282 TrpGlnPro-----GlyAlaIlaTyrLeuTyrGlnLeuIleGlnIleValanine 296
Db 875 TGGTAGCCGTTACTGTGACGAAACCCCTGCTACTGTGATTCATGAGTCAGCTG 934
QY 297 ValGly-----SerSerGlyAspValValAspThrTyrAlanLeuIleValGlyValG 314
Db 935 ACTGCCACAGGCTACTGGGCCGCTGCTGACTCTACACTCCCTGGGGATCCG 994
QY 315 ThrValIysValIalAgiLysSerGlnPheLeuIleAsnGlyLysProPheThrHrgly 334
Db 995 ACTGAGCTGTCACCAAGAGTCAGTCCTCTCAATGGAAACCTTCTATTCACGGT 1054
QY 335 PheGlyLysIleGluAspThrIleValArgGlyLysGlyLysAspProAlaTyrMetVal 354
Db 1055 GTCAACAGCTGAGCTGAGGATGGCGACATCGAGGAAGGGCTTGAGCTGGCCCTGCTGGT 1114
QY 355 HisAspSerGlnLeuMetLysSerIlePheGlyAlaAsnSerPheArgThrSerHistYPro 374
Db 1115 AAGGACTTCACCTCTGTCGGCTGGTCAACGCTTCCGTRACCAAGCTCCC 1174
QY 375 TyrAlaGluGluValMetAspPheAlaAspPheAlaAspArgAsnGlyIleLeuValIleAspGluThr 394
Db 1175 TATGCGAGGAGTGTGAGCAGTCAGTCAGCTGAGCTTGGGATGTCATGATGATG 1234
QY 395 ProAlaValGlyLeuAlaIleAlaLeuMetGlyValSerGlyAlaProGlnThr 414
Db 1235 CCCGGCTGCGCCCTGCGCT 1264
QY 415 PheThrProAspAlaIleAspAspLysThrGlnGluAlaLysGlnAlaIleArgGlu 434
Db 1265 TIC-----ArgAGCTTCTGTCATCACCCATGAGGTTGGAGA 1309
QY 435 IleuIleAlaArgAspLysAsnAlaSerValValMetTrpSerIleAlaArgGluPro 454

Db	1310 GTGGTTCGTTGGACAGAACACCCCCGGCTGTGTTGGCTGTCGACAGAGCCT 1369	ORIGIN	
Qy	455 AlasRhiSgluaspGlyIvaArgGlutPheLeuThrAsnLeuThrArgLln 474	Alignment Scores:	
Db	1370 GCGTCCACCTAGATCTCTGCTACTACTT-GAA----- 1404	Pred. No.:	2.62e-120
Qy	475 LeuAspProThrArgProlethrPheAlaAsnValGlyInAlaThrTygInLeuAsp 494	Score:	1175.00
Db	1405 ----- 1413	Percent Similarity:	55.92%
Qy	495 ArgLeSerAspLeuPheAspValSerCysLeuAsnArgTyPheGlyTyPheTyserGln 514	Best Local Similarity:	41.28%
Db	1414 -----GTCGATGPGATCTGTTGAAGCCTACTCTTGATCACGAC 1458	Query Match:	35.03%
Qy	515 ThxGlyAspLeuGluGluAlaGluAlaLeuGluLysGluLeuHisGlyTrpInGlu 534	DB:	6
Db	1459 TACGGGCACCTCGTCACTGATCTGCTGAGCTGAGCACCACCGTGTGAGAATGGTATAAG 1518	Gaps:	12
Qy	535 LysPheHiSArgProleValMetThrGluTyrglyValaspThrLeuAlaGlyLeuHiS 554	US-10-757-093-4 (1-634) x CD014092 (1-1995)	
Db	1519 AspGATCAGAAGCCATTATCAGGGAGAGTCAGGACATTGAGCTTCAC 1578	Qy	42 ProGlnArgThrSerSerArgGluLeuValAsnLeuGluPheLeuIle 61
Qy	555 SerIleLeuGlyLeuProTrpSerGluGluPheGlnValGlnMetLeuAspMetTyRHS 574	Db	101 CCCAGGAGGCCGCGTCGGGGAGTCAGCTGAGCTGAGCCCTCTGGACCTC----- 154
Db	1579 CAGGATCACCCTCTGATGTACTGAGAGAGAACGAGACAGCACTGAGCTAACAGACTACAT 1638	Qy	62 AlaSerGlyLeuAsnLeuPheHiSArgProleValMetLeuAspMetTyRHS 574
Qy	575 ArgValPheAsp-----ArgIleGluSerMetAlaGlyGluHiSValTrpAspHeAla 592	Db	155 CGGCCGACTCTCTAACACCGACGCCGGCGCTTGAGGAGCTGGTACCGGGCG 214
Db	1639 CTGGGTTGGATGAAACAGGAGAMATACTGGTTGGAGAGCTATTGGATTTCAC 1698	Qy	76 LeuProArgGly-----LeuGluCysProValProLeuAsnLeuPhe 92
Qy	593 AspPheGlnThrAspLeuGlyIleLeuGlyValAspGlyAsnGlyLeuGlyValPheHr 612	Db	215 CTGTGGAGTAGGCCACCGGGAGACCCAGTCCTCCACCTCATGACATCGC 274
Db	1699 GATTTGATGACTGAACTGACAGTCGACGAGAAAGTGCGAGGTCCTTGCGAGAGAT 1758	Qy	93 IleSerArgGluIleHiSAspHiSValGlyTyPvalTyTyrglnArgGluValLeuI 112
Qy	613 ArgAspArgIysProLySalaAlaAlaIleSerLeuArgAlaLaaqrThrSerIle 631	Db	275 CAGGATGCCCTCGGGCATTTGTCGCTGCTGGTACGACGGAGGTATCTG 334
Db	1759 CGGGCAGAGACACCAAAGTGCGAGGTCCTTGCGAGAGATCTGGAGATT 1815	Qy	113 ProLeuGlyTyPserGlnGluArgTyrglyValAralaGluUserAlaThrHiSgly 132
RESULT 3			
CD014092		Db	335 CGGACGATGACCCAGAC----- 355
LOCUS	CD014092 90134967 Single gene library 1995 bp mRNA 1995 bp mRNA 1995 bp mRNA sequence.	Qy	133 ArgLeTyryValAsnAsnArgLeuValAlaGluHiSValGlyGlyTyTyrrProheGlu 152
DEFINITION	90134967 Single gene library Homo sapiens cDNA, mRNA sequence.	Db	356 -----CTGCCACACAAGAGTCG----- 373
ACCESSION	CD014092	Qy	153 AlaAspPvalThrGluLeuValAlaProGlyGluLysPheArgLeuThrIleGlyValAsn 172
VERSION	CD014092.1 GI:37777621	Db	374 ----- 391
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SOURCE	Homo sapiens (human)	Db	392 CATC-CTAGCCATCGGCTGCTCCAG-GT-TACTTT-----CTGAGGATTGCGAGTCGCC 391
ORGANISM		Qy	193 LysArgIleGlnThrTyrglyHiSAspPheTyrsAspTyraGlyLeuAlaArgSerIle 212
REFERENCE		Db	429 -----GTCAGAACACATATTGACTTTCACTTCACTGCGACTGCAAGGGCTGTGA 482
AUTHORS	Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R., Au-Young,J. and Stuve,L.L.	Qy	213 TrpLeuIleThrHiSgluThrLeProProGlyLysIleThrThrGlyAspAlaThrGly 232
TITLE	PCR isolation and cloning of novel splice variant mRNAs from known drug target genes	Db	483 CTCTGTRGACGACACCAACCTACATCGATGACTCACCGTCACCAACCGCTGGAG 542
JOURNAL	Genomics 83 (4), 566-571 (2004)	Qy	233 GlyAspAsnGlyLeuIleAsnTyrglyValAluGluValAlaAenglnThrIleGlyIle 252
COMMENT	Contact: Jin, P. Incyte Corporation 3160 Porter Drive, Palo Alto, CA 94304, USA Tel: 650 621 8639 Fax: 650 621 8965 Email: pjin@incyte.com	Db	543 CAAAGACAGCTGGCTGIGGATTAACAGATCTCTGTCAGGGCAGTAACCTGTCAGTG 602
FEATURES	Location/Qualifiers	Qy	253 GluIleSerValIleAspGluAspGlyIvalIleValAlaIleAsnIleValGly----- 602
source	1. i195 /organism="Homo sapiens" /mol_type="mRNA" /db_xref=taxon:9606" /clone lib="Single gene library" /note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."	Db	603 GAAATGGCTCTTGTGATCGCGAAGAACAGTCGTCGCGATGGACTGGGACCCAGGG 662
		Qy	273 ThrValThrIleProSerValIleLeuIlePro-----GlyAlaIla 287
		Db	663 CAACTTAAGGAGGCCAGTCGACGCTCTGCGCTACCTGATGCAAGACGCCCTGCC 722
		Qy	288 TyrLeuTyrglyInLeuGluValAlaAsnIleValGly-----SerSerGlyAspValValAsp 305
		Db	723 TATCGTATCATGGAGCTGAGCTGATGAGACCTACAGGCGCTGCTGTCAC 782
		Qy	306 ThrTyFAsnLeuAlaThrGlyValArgTyryValAlaIleAsnGlyLeuPheLeuIle 325
		Db	783 TTCTACACATCCCTGTCGGAGATCGCACTGCTGTCGTCACCAAGGCCAGTCCTCATC 842
		Qy	326 AsnGlyLysProPhoTyrrPheGlyPheGlyLysHiSgluAspThrAlaValArgly 345

		ORGANISM
Db		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Qy		REFERENCE
Db	903	AUTHORS
Qy	346	Carninci, P. and Hayashizaki, Y.
Db	903	JOURNAL
Qy	366	High-efficiency full-length cDNA cloning
Db	963	Meth. Enzymol. 303, 19-44 (1999)
Qy	386	Method. Enzymol. 303, 19-44 (1999)
Db	406	1023
Qy	406	TATGGGATGTGCTCATCGATAGTCACCGTCACTCCATGCGAGGAGTGATGCAATGTCGACCGC
Db	406	386
Qy	406	ArglylilevalValleAspGluThrProAlaProIvaValgylevanlieAlaLeuMetGly 405
Db	406	1023
Qy	406	TATGGGATGTGCTCATCGATAGTCACCGTCACTCCATGCGAGGAGTGATGCAATGTCGACCGC
Db	406	386
Qy	406	1071
Db	406	--CCGAGTCCTC-----ACAACCTTTCTG 1097
Qy	426	1071
Db	426	GlualahislyGlnalalleArgGluleureLalaargaspybsnhislaserval 445
Qy	426	1098
Db	426	CATCACCATGATCAGGAGTAGGAGAAGCTGGCGTAGGAGAACACCACCCGCSC 1157
Qy	446	446
Db	446	ValMetProSerLeaAlaArgluProAlaSerHisGluArglylalaArgluTyvPhe 465
Qy	446	1158
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Qy	446	466
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Qy	486	1218
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Qy	486	1272
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Db	506	ArgArgTyvPhglyTyPTyserGlnlhrGlyAspLeuGlugluAlaLeu 525
Qy	526	1392
Db	526	GluLybGluLeuHiGlyTpoGlnGlySphehisArgProleValMetThrGluTyv 545
Qy	526	1392
Db	526	GCAACCGAGTTGAGAATGTTAGAGATTCAGAGCCATTATCAGCGAGAT 1451
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Db	546	GlyAlaLeptHeuAlaGlyLeuHiSerLeuLeuglyLeuProTpSerGluGluHe 565
Qy	546	1452
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Qy	604	1692
Db	604	ArgGlyAsnLeuValGlyValpheThArgParglySpolySalaAlaAlaHiSer 623
Qy	604	1692
Db	604	CAGGGGATAAAGGAGTCCTACGGCAGAGCACCAAAGTCACCGTCTCCT 1691
Qy	624	624
Db	624	LeuArgIlaArgTrpHsrSerle 631
Qy	624	1692
Db	624	TTCGAGAGAGAGACTGGAGAAT 1715
RESULT 4		COMMENT
AK041058	AK041058	Submitted (16-JUL-2001) Yoshihiko Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan; E-mail: genome.ref@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
DEFINITION	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone A530072005 product;beta-glucuronidase structural, full insert sequence.	Please visit our web site for further details.
ACCESSION	AK041058	URL: http://fantom.gsc.riken.jp/
VERSION	AK041058.1	Location/Qualifiers
KEYWORDS	HTC; CAP trapper.	Source
SOURCE	Mus musculus (house mouse)	organisms="Mus musculus"

/mol_type="mRNA"
 /strain="CE7BL/6J"
 /db_xref="RANTOM DB:A530072005"
 /db_xref="Taxon:10090"
 /clone="A530072005"
 /sex="male"
 /tissue type="sorta and 'vein'"
 /clone_1="RIKEN full-length enriched mouse cDNA library"
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 /note="beta-glucuronidase structural (MGP|MGI:95874,
 GB|NM_010568, evidence: BLASTN, 99%, match=733)
 putative"
 2265.
 /note="putative"
 2274
 /note="putative"

ORIGIN

Alignment Scores:
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 Score: 1.68.50 Matches: 249
 Percent Similarity: 55.76% Conservative: 90
 Best Local Similarity: 40.95% Mismatches: 179
 Query Match: 34.84% Indels: 90
 DB: 3 Gaps: 13

US-10-757-093-4 (1-634) x AK041058 (1-2274)

Qy 42 ProGlnArgThrSerSerArgGluLeuValAsnLeuAspGlyLeuTrpAspHealaLeu 61
 Db 101 CGAAAGAGAGGAGCCGTCGGAGCTCAGGCTGGACACTGGCACTTCCGCC 160
 Qy 62 -----AlaSerGlyLeuAsnAspThrAlaLglnProTrp--ThrAlaProLeuPro 77
 Db 161 GACCTCTGAAACAAACCGGCTGGAGGGTTGACGAGCATGGTACCCGGCAGGGCTGG 220
 Qy 78 LysGly-----LeuGlycysProValProAlaSerTyroAspPheGlnLeuMetLysTrpIleGly 94
 Db 221 GAGCGGGCCCACCTCTTGACAGCCTCTCCCTCTAGCTTCATGACATCACCCAGAA 280
 Qy 95 ArgGluLeHisAspHsValGlyTPValTrpTrpGlnAGluValleValProlys 114
 Db 281 GGAGCCCTGCGACTTTATGCTGAGTGCTGAGCTGAGCTGGCAACGGTACTTCGGCA 340
 Qy 115 GlyTrpSerGluGlu-----ArgTyroLeuValArgAlaGluSerAlaThrHis 131
 Db 341 CCGTGGACCCAAAGATACCGGACAAGCTGAGCTGGGTGAGGATCACGTGCC---CAITAT 397
 Qy 132 GlyArgIleTyroValAsnAspLeuValAlaGluHisValGlyGlyTyThrPrope 151
 Db 398 TAGCAGITGTGTGTATCCAA----- 418
 Qy 152 GluAlaaspValThrGluLeuValAlaProGlyGluLys_PheArgLeuThrIleGlyVa 171
 Db 419 -----GCGTTACATTGCTGTCAGACAGCTT----- 446
 Qy 171 LysAsnAspGluLeuThrHisGluThrIleProProGlyLysIleThrThrGlyAsnAlaTh 191
 Db 446 ----- 446
 Qy 191 rGlyLySArgIleGlnThrTyGlnHisAspHpheTyAsnTyValAlaLgln 211
 Db 447 -----GACTCTGCACTGCGGACTCATGCTG 478
 Qy 211 rIleTriepleutSerValProGlnGlnHistIlegInAspIleThrValValThrAspVa 231
 Db 479 TCTGTCCTCTTACACCCCTTACACTCTACGATGATCTGACTTA 538
 Qy 231 LaspGlyAspArgGlyIleLeuAsnTyGluValGluValAlaAsnGlnThrThrGlyGly 251
 Db 539 GAGGAGAGACataggctggacactctgttttcgtgggggggtGacaATTC 598

Qy 251 nIleGlnIleSerValIleAspGluAspGlyAlaIleValAlaIleAspGlyAlaGly 271
 Db 599 GCTAGAACTGCACATTTGGATGAGGGCTGCAAGTCGTCAGGACAGGGACCA 658
 Qy 271 nGlyThrValThrIleProSerValIleLeuTrpGlnPro-----Glyal 286
 /note="beta-glucuronidase structural (MGP|MGI:95874,
 GB|NM_010568, evidence: BLASTN, 99%, match=733)
 putative"
 2265.
 /note="putative"
 2274
 /note="putative"

Qy 306 RTyrAspLeuAlaThrGlyValArgThrValIysValAlaGlySerGlnIleHeleIleAs 326
 Db 776 CTACACCCCTCTTATCGGATTCGAACAGTGCGCTGTCACAAAGGCAAGTCATAA 835
 Qy 719 AGCTACAGIAGTACTCTTGGAGGTGAGGACACAACTGACTGCTGAGCTA 775
 Db 836 CGGAAAGCCCTCTTATTCAGGCTCAATAAGCCAGGATTCAGATTCGGAGGA 895
 Qy 346 sGlyHiAspProAlaTyroMetValHiAspPheGlnLeuMetLysTrpIleGly 366
 Db 896 AGGCTTGACTCGCCGCTGCTGTAAGGANTTCACCTGCTCGTGCCTGCGGGCAA 955
 Qy 366 nserPheArgThrSerHistYrProTyPheThrGlyPheGlyLysGluValAspPhe 386
 Db 956 TTCTTGTGACCAAGCCACTAACCCCTACTACAGGAGGTTACTTCAGCTCTGACCATA 1015
 Qy 386 nGlyLeuValValAspGluLeuProAlaValAlaGlyLeuAsnIleAlaLeuMetGly 406
 Db 1016 CGGGATTTGGGTCATCGTAGTGTGTCGCGGTGGCGCATCTGCTA----- 1061
 Qy 406 1SerGluSerGlyAlaProGlnThrPheThrProAspPheAlaLeuAspLysThrGlnG 426
 Db 1062 -----CTCTAGAGTTTGGCAACGGTACTTCGGCAC 1094
 Qy 426 uAlaHisIleGlnAlaIleArgGluLeuIleAlaLglnAspIysAsnHiIleSerVal 446
 Db 1095 ---CACTTAGGAGGTGATGGAGGAGCTGTCGCCGGACAAATCACCCTGCGGTR 1150
 Qy 446 1MetTpSerIleAlaAsnGluProAlaSerHiGluAspGlyAlaArgGluTyPheG 466
 Db 1151 GATGTCCTCTGGCCAAATGAGCCTTCTCTGCTGCTGAGAACCGGGCGCATTTAA 1210
 Qy 466 upRoleThrAsnLeuThrArgGlnLeuAspProThrArgProleThrPheAlaAsnVa 486
 Db 1211 GACGCTGATCACCCACACAAAGCCGCTGACCTCACCGTCCCGGACCTT-----GT 1264
 Qy 486 IGLYTHALATHTyrglnIeuAspArgIleSerAspLeuPheAspValSerCvleas 506
 Db 1265 GAGCAACGCCAAATATGATGCGAGACCTGGGGCCCCGTACTGGATGTTACTGIGTAA 1324
 Qy 506 nArgTrpPheIleTyroTyrsErGlnThrGlyAspLeuGluGluAlaLalaLeuG 526
 Db 1325 CAGCTACTTCCTGCTGATCAGACTATGGCCATTGGAGCTGATGATC 1384
 Qy 526 wlyGluLeuHiGlyTrpGlnGlyLysPheHiAspPheAspProLeuValMetThrGluTrpG 546
 Db 1385 TAGCAGTTGAGCTGATGATAAGCGCATGAGCCATTATCCAGCGAGTATG 1444
 Qy 546 YalaAspPheAlaGlyLeuIleSerIleLeuGlyLeuProPheSerGluGluPheG 566
 Db 1445 ACCAGCCAACTCCAGGATCCACAGGACCTGCTGAGCTGAGGAGTACCA 1504
 Qy 566 nvalGlnMetLeuAspMetTyRhiArgValPheAsp-----ArgIleGluSerMetAl 584
 Db 1505 GAGGGTCTGAGAAATACCATGAGTCGTCGAGTCAGAAAGATACTG 1564
 Qy 584 aglyGluLeuValTrpAspPheAspPheGlnThrAsnIleGlyIleLeuG 604
 Db 1565 CGGAGAGCTCTGCGAAATTGCGGACTTCATGAGCAACAGTCACCCCTGAGTA 1624
 Qy 604 pglyAsnLysLysGlyValPheThrArgAspArgLysProLysAlaAlaLalaIle 624

Db 1625 CGGAACAGGAGGGGACTTCACTGCCAGGAGCACCCAAACTTGSCCTTATT 1684
 Qy 624 uRglaArtpThrSerIle 631
 Db 1685 GCGAGAGATCTGGGATT 1706

RESULT 5

Db 1625 CGD014093 1853 bp mRNA linear EST 21-OCT-2003
 Locus 90135266 Single gene library Homo sapiens cDNA, mRNA sequence.
 Definition CD014093 CD014093.1 GI:37777622
 Accession CD014093
 Version EST:
 Keywords Homo sapiens (human)
 Source Homo sapiens
 Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Reference 1 (bases 1 to 1853)
 Authors Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
 Title PCR isolation and cloning of novel splice variant mRNAs from known
 drug target genes
 Journal Genomics 83 (4), 566-571. (2004)
 Comment Contact: Jin, P.
 Incyte Corporation
 3160 Porter Drive, Palo Alto, CA 94304, USA
 Tel: 650 621 8639
 Fax: 650 621 8965
 Email: pjin@incyte.com.

FEATURES

Source

1. .1853 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_id="Single gene library"
 /note="Vector: pDrive Cloning Vector; RT-PCR was performed
 using gene-specific primers flanking the open-reading
 frame. PCR products were subcloned into pDrive Cloning
 Vector and sequenced completely using M13 forward and
 reverse primers. Sequencing gaps were closed by
 re-sequencing using primers flanking the gapped areas."

ORIGIN

Alignment Scores:

Pred. NO.:	8.53e-106	Length:	1853
Score:	1045.50	Matches:	227
Percent Similarity:	50.90%	Conservative:	84
Best Local Similarity:	37.15*	Mismatches:	159
Query Match:	31.17*	Indels:	141
DB:	6	Gaps:	13

US-10-757-093-4 (1-634) x CD014093 (1-1853)

Qy 42 ProGlnArgLysSerSerArgGluLeuValAsnLeuAspGlyLeuTrpPheLeu 61
 Db 101 CCCAGGAGGAGCCGTRGGAGTCGAAGGGCTGGACGCCCTCGAGCTTC----- 154

Qy 62 AlaSerGlyLeuAsnAspThr-----AlaGlnProThrAlaPro 75

Db 155 CGCGCGCACTTCTGACAACAGGCCCGGGCTGAGGAGCAGGTGCTACGGGGCG 214

Qy 76 LeuProLysGly-----LeuGlucySProValProAlaSerTyraAspIlePhe 92
 Db 215 CTGGAGGAGTCAGGCCAACGGTGGACATGCCAGTCCTCCAGCTCATGACATCAG 274

Qy 93 IleSerArgGluLeuIleAspPheSValGlyLysPheValTyrglArgLysValLeuLeu 112
 Db 275 CAGGACTGGCGCTGCGGCATTTGCGCGCTGGAGTCGAACGGAGCTGATGCTG 334

Qy 113 ProLygLyTpsSerGlnGlu-----ArgTyruLeuValArgLysSerAlaThr 129
 Db 335 CGGGAGCGATGGACCCAGGACCTGGCGACAAGAGTGTGCTGAGGATTGGCAGTGCC--- 391

Qy 130 HisHisGlyArgIleTyrValAsnAsnArgLeuValAlaGluHisValGlyGlyTyrrThr 149
 Db 391 ----- 391

Qy 150 ProheGluIlaAspValThrGluLeuValAlaProGlyGlyLysPheArgLeuThrile 169
 Db 391 ----- 391

Qy 170 GlyValAlaAsnGluLeuThrHisGluThrProProGlyLysIleThrThrGlyAsn 189
 Db 392 ----- 392

Qy 190 AlaThrGlyLysBargIleGlnThrTyrglHisAspPheTyrasTyralaGlyLeuAla 209
 Db 393 ----- 393

Qy 210 ArgSerIleTrpLeuTyrservalProGlnDlnHisIleGlnAspIleThrValThr 229
 Db 404 ----- 404

Qy 230 AspValAspGlyAspAspGlyIleLeuAsnTyrgluValGluValalaAsnGlnThrThr 249
 Db 410 ----- 410

Qy 250 GlyGlnLleGlnLeSerValIleAspGluLysPheGlyAlaValAlaLysAlaSerGly 269
 Db 452 TTCAGCTTGAGTGGCTCTTGGATGAGCAGAATGGCTCTGCGGAATGGACTGG 511

Qy 270 AlaGlnGlyLysThrLeuThrIleProSerValValysLeuTrpGlnPro----- 284

Db 512 ACCCAEGGCCAACTTAAGGCCAGGTCTAGCCCTCTGGCGCCGTRACTCATGACAA 571

Qy 285 GlyAlaAlaTrpLeuTyrglnIleGlnValAlaValAlaLysAlaSerGly 302
 Db 572 CGCCCTGCCTACTGATCTGATCTGATCTGAGCTGACTGACCTGACTGCGCT 631

Qy 303 ValValAlaPheThrTyrsValLeuAlaThrGlyValArgThrVallyValAlaGlySerGln 322
 Db 632 GTCGTCGACTCTCACACACCCCTGGGGTCCGACTGCGCTTCACCAAGGCCAG 691

Qy 323 PheLeuIleAsnGlyLysProHeptYrPheThrGlyPheGlyLYHisGluAspThrAla 342

Db 692 TTCTCTCATGGAAACCTTCTTACCTGCGCTACGGGTGTCACAGCATGAGGATGGGA 751

Qy 343 ValArgGlyLysGlyHisAspProLysTyrMetValHisAspPheGlnIleMetLysTP 362
 Db 752 ATCCGAGGGAAGGGCTTCGACTGGCGCTGCTGGAGGCTTCACCTGCTTCG 811

Qy 363 IleGlyAlaLysSerPheArgThrSerHistYrProTyralaGluGluValMetAspPhe 382
 Db 812 CTGGGTCACGCCCTCCACGCCCTACCCCTATCCAGACAGAGCTGGAGATG 871

Qy 383 AlaAspArgAsnGlyIleValValIleAspGluThrProIleValGlyLeuAsnIleAla 402
 Db 872 TGTGACGCCATGGGATTGCTGTCATGAGTAGTGTGCCCGCGCTGGCGCTG--- 928

Qy 403 LeuMetGlyIvalSerIleGlyIvalProGlnThrPheThrProAspAlaIleAsp 422
 Db 929 ----- 929

Qy 423 LysTrpGlnGluAlaIleIleAspGluLeuIleAlaArgAspIleAla 442
 Db 947 GTTCCTCTGCATCACACATCAGCTGAGTCAGGAGCTGCTGCCGAGGACAC 1005

Qy 443 AlaSerValIvalMetTrpSerIleAlaIleGluProAlaSerHisGluAspGlyAlaArg 462
 Db 1007 CCCGGCGCTGCTGATGCTGCTGCGCCARAGGAGCTGCTGCCAGCTGCTG 1066

Qy 463 GluTrpPheGluProLeuThrAspLeuThrArgGlnIleAspProThrArgProIleTrp 482
 Db 1067 TACTACTGAGATGCTGCTCACACCAAATCTTGCGACCCCTCCGCCCTGACC 1126

Qy 549 ThrlleualgylLeuhisserleLeuglytauprotPseqglugupheGlnvalgln 568
 Db 910 AGGATTCAGGTTTACAGGATCCACCTCTGATGAGTACAGAAGTACCAAGAAGT 969
 Qy 569 MetLeuAspMetTyRhisargValpheAsp----ArgIleGluSerMetAlaGlyGlu 586
 Db 970 CTCCTAGAGCACTTACCTCTGGCTCTGATCAAACGAGAAATCTGCTGGAG 1029
 Qy 587 HisvalTrpAspPheAlaAspPheInThraLeuLeuglyIleLeArgValaspGlyAsn 606
 Db 1030 CTCTTGGAAATTGGCCTGATGACTGACAGTCACCCACGAGAGTGCTGGGAAT 1089
 Qy 607 LysLybGlyValPhenTrpArgPheAspLysPolyGalaAlaAlaIleSerLeuArgAla 626
 Db 1090 AAAGAGGGATTCCTCATGGAGACACAAAAGTGCAGCTTGTGGAG 1149
 Qy 627 ArgTrpThrSerIle 631
 Db 1150 AGTACTCGAAGATT 1164

RESULT 7

CD503076 LOCUS CD503076 1124 bp mRNA Linear EST 12-JUN-2003
 DEFINITION CD460-C07 5', mRNA sequence.
 ACCESSION CD503076
 VERSION CD503076.1 GI:3132977
 KEYWORDS EST,
 SOURCE
 ORGANISM Gasterosteus aculeatus (three spined stickleback)
 Butariofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 Acanthomorpha; Acanthopercyli; Percormorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.
 1 bases 1 to 1124)
 AUTHORS Kingsley, D.M., Peichl, C., Balabhadra, S., Grimwood, J., Dickson, M.,
 Schmutz, J. and Myers, R.M.
 TITLE Unpublished sequence tags from Gasterosteus aculeatus
 JOURNAL Contact: Kingsley, DM
 COMMENT HMM and Department of Developmental Biology/
 Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
 Tel: 650 725 5954
 Fax: 650 725 5939
 Email: kingsley@cmgm.stanford.edu
 Plate: 60

High quality sequence stop: 782.

Location/Qualifiers

Source 1. .1124
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /Strain="Saline river, CA"
 /db_xref="taxon:6993"
 /clone="CD460-C07"
 /sex="mixed male and female"
 /tissue_type="heads and internal organs combined"
 /der_stage="adult"
 /clone_id="SHC-CDA"
 /notec="vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI (5' adaptor); Site 2: XbaI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo dT sequence preceeded by a synthetic XbaI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."

FEATURES

ORIGIN

Alignment Scores:
 Pred. No.: 7.26e-79 Length: 1124
 Score: 803.00 Mat chns: 164
 Percent Similarity: 60.74% Conservative: 48
 Best Local Similarity: 46.99% Mismatches: 115
 Query Match: 23.94% Indels: 23
 DB: 6 Gaps: 5

US-10-757-093-4 (1-634) x CD503076 (1-1124)

Qy 284 ProGlyValAlaTyreLeuTrpValLeuGluAlaValLeuGlySerGlyAspVal 303
 Db 8 CGCAACCCAGGTACCTTACTCTCTGGAGTGTGCTTACTGCTGAGGATCTGCT 67

Qy 304 Val--AspThrTyrAsnLeuAlaThrGlyValArgThrValGlySerGln 322
 Db 68 TCCAACGAGGAGTACACTCTAACAGCTGCTGGCTGGGAGGTTACCGAGACCGAG 127

Qy 323 PhelLeuIleAsnGlyLysProPheTyrPheTerGlyPhyGlyBisGluAspThrAla 342
 Db 128 TTCTCATCACACAAAGCCCTCTACTTCCACGGAGTAATAACGAGGACTGTAT 187

Qy 343 ValArgGlyLysGlyMysAspProAlaTyrmValHisAspPheGlnIleMetLysTP 362
 Db 188 ATTGGAGGCAAAAGGCCCTCATGGTGAAGGACTTAACTTACTCTTGAGTGG 247

Qy 363 IleGlyAlaAsnSerPheArgThrSerHistYrProTyraLalaGluGluValAlaGlySerGln 322

Db 248 TGGGGCCCAACTCTGGCTGGCAGGACCTACCCCTATGGAGGAGGATCTGGAGATG 307

Qy 383 AlaAspArgAsnGlyIleValValIleAspGluIleProAlaValGlyLeu--AsnIle 401

Db 308 TGTGACGCCGCGCAGGCGATGAGTAGCCAGGTGCCCCGCGCTGGACATAAAGACATT 367

Qy 402 AlaLeuMetGlyValSerGlyAlaProGlnThrPheThrProAspAlaSer 421

Db 368 CCCAGTTGCA-----379

Qy 422 AspLysThrGlnGluAlaIleGlyGlnAlaIleArgGluIleAlaGlyAspLysBsn 441

Db 380 AACGCCCTTAAACCATCACGGTGTGATGAGGAGCTGGTACCTGGAGAC 439

Qy 442 HisAlaserValValMetTrpSerIleAlaLnsGluProAlaSerHisGluAspGlyAla 461

Db 440 CATCCCTCTGGCTGTCATGGCTAGGCCATGAGGCCGCTGAGATGCCCTCTGCT 499

Qy 462 ArgGlyTrpPheGluProLeuThrAspLeuAspProTrpArgProle 481

Db 500 GATTCTTCAAACTCTGATAAACTACCAAGAATGGATCAACCGGCCGTC 559

Qy 482 ThrPheAlaAsnValGlyIleThrAlaThrYrgIleLeuAspGlyLeuSerAspLeuPheAsp 501

Db 560 ACTTT---ATCACAGACAGTAATCCAGGATTAAGGGCTCCCTACGTCAC 613

Qy 502 ValSerCysIleAspArgTrpPheGlyTrpTrpSerGlnIleArgPheGluIala 521

Db 614 GTCATCTGGTAACAGTACTCTCTGGTACCATGAGCCGGCACCGAGGTCTC 673

Qy 522 GluAlaAlaLeuGlyLeuIleIgylTrpGlnGlySerPheIleAspProVal 541

Db 674 CCCATCAGCTCAACACTACTCTGGAGACTGCTGGTACCATGAGAACCCATCTC 733

Qy 542 MetThrGlyTrpGlyAlaAspThrLeuAlaGlyLeuIleSerIleLeuGlyLeuProPr 561

Db 734 CAGGGGATACGAGGGATGCGGTCGGGCTCAGTGCACCCGTTGATGTT 793

Qy 562 SerGluGluIpheGlnValGlyMetLeuAspMetTyRhisargValPheAsp----Arg 579

Db 794 ACTGAGGAGTACAGAGGTAGTCTCTGGAGCTACCAACAGCTGTCAGGAGAAAGG 853

Qy 580 IleGluSerMetAlaGlyGluIleValTrpAsnPheAlaSpHedGlnThrAsnLeuGly 599

SAIL_443_B06.v2, genomic survey sequence.	ACCESSION
CL467845	CL467845
GSS:	GI:45965487
ORGANISM	Arabidopsis thaliana (thale cress)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliopsida; eudicots; Brassicales; Brassicaceae; Arabidopsis; 1 (bases 1 to 921)
AUTHORS	Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bawden,J., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Mignel,T., Hutchison,D., Kimmerly,B., Mizell,T., Katigiri,F., Glazebrook,J., Law,M. and Goff,S.A.
JOURNAL	Plant Cell 14 (12), 2985-2994 (2002)
PUBMED	12236987
COMMENT	Contact: Sessions A Applied Trait Genetics Syngenta Biotechnology Inc. 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com
FEATURES	source
ORIGIN	1. .921 'organism="Arabidopsis thaliana"' 'mol_type="genomic DNA"' 'ecotype="Columbia"' 'db_xref="taxon:3702"' 'clone="SAIL_443_B06_v2"' 'clone_lib="SAIL Collection"' 'note="T-DNA left border Sequences were isolated using a modified TAIL-PCR strategy'"
ALIGNMENT	scores: pred. No.: 2.51e-78 Score: 797.00 Length: 921 Percent Similarity: 76.45% Matches: 154 Best Local Similarity: 63.64% Conservative: 31 Query Match: 23.76% Mismatches: 54 DB: Indels: 3 Gaps: 2
US-10-757-093-4 (1-634) x CL468645 (1-921)	RESULT 10
QY 388 IleValIvalleAspGluThrProAlaValGlyLeuAsnLeuAlaLeu--MetGlyVal 406	CD503098 LOCUS CD503098 1118 bp mRNA linear EST 12-JUN-2003 DEFINITION CD50-D07.x1d-t SHGC-CDA Gasterosteus aculeatus cDNA clone CD50-D07 5, mRNA sequence.
Db 793 ATCGTGGATGATGAGAACTCCCTCTTAGCATGGTTC 734	CD503098 VERSION CD503098.1 GI:31433153
QY 407 SerGluSerGlyAlaPro---GlnThr-Phenyl-Pro-PheAlaIleAspAspSerThrGln 425	KEYWORDS EST, Gasterosteus aculeatus (three spined stickleback) ORGANISM Gasterosteus aculeatus
Db 733 GAAGGGCACACAGCGAAAGAACGCTACAGGGAGGGCACTCAAGGGGAACTCA 674	REFERENCE 1 (bases 1 to 1138) AUTHORS Kingsley,D.M., Peichel,C., Balabandra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M. TITLE Unpublished sequence tags from Gasterosteus aculeatus JOURNAL unpublished (2003) COMMENT Contact: Kingsley, DM HMB and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA Tel: 650 725 5954 Fax: 650 725 7739 Email: kingsley@cmgm.stanford.edu Plate: 60 High quality sequence stop: 782.
QY 425 nGluAlaIleGlyGlnAlaIleArgGluLeuIleAlaArgAspLysAsnHisAlaSerVa 445	FEATURES source
Db 673 GCAGCGGACTTACAAGGGATTAAAGAGGTGATAGCCGTGACAACCCACCAAGCT 614	1. .1138 'organism="Gasterosteus aculeatus"' 'mol_type="mRNA"' 'strain="Salinina river, CA"' 'db_xref="taxon:69293"' 'clone="CD460-D07"' 'sex="mixed male and female"' 'tissue_type="heads and internal organs combined"' 'dev_stage="adult"' 'clone.lib="SHGC-CDA"' 'note="Vector: Lambda ZAP Express/pBK-CMV; Site 1: EcoRI (5' adaptor); Site 2: Khol (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with
QY 445 IVALMetrTrPSeIleAlaAsnGluProLaserThrIleGluAspGlyAlaArgGluLysPh 465	493 TCTAATGTCGCGAGCGTACACCGGATACCATCAGCGATCTTGTGCGCTGCGCT 433
Db 613 GGGATCTGGAGATTCGCCAACGACCGATACCGCTCGACGGCAAGGGCACGGAATT 554	505 easNarQTYRPhiGlyTrpTyrSerGlnThrGlyAspLeuGluGluAlaGluAlaAla 525 Db 373 GRACCTTATTACGGATGGTAGTCGCAAAGGGGATTGGAAACCGCAGGAAGGTA 374
QY 465 egluProleuthAsnLeuGluGlnLeuAspProProAspProLeuThrPheAlaAs 485	525 uGluIysGluLeuHiGlyTrpGluGluIysPhiHiSArgProLevalMetThrLeuY 545 Db 373 GGAAGAGAACTTCAGCCAGGAGATTGCACTACGGATTCATCACCGATA 314
Db 553 CGCCCACTGGCGGAAGCAAGCGCTAACTCGACGCCAGGCGTCGATACCTCGCTCA 494	565 eglyIalaAspThrLeuIaGlyLeuHiSerLeuIgIleAspArgIleGluSerMetAlaI 585 Db 253 TCAGTGCGATGGCTGATATGATCACGGCTCTGTGCGTCAGGGCGTCGTCGG 194
QY 485 nVALGlyIthrAlaThrTyrglnLeuAspArgIleSerIlePheAspValSerCysI 505	595 yGluIvaIvlTrpAsnPhelaAspHeGlnThrAsnLeuGlyIleLeuGluAspG 605 Db 193 TCAACAGGTGTTGAATTCGCGATTGCGACCTCGCAAGCGATATGCGCTGGCG 134

Query Match:		21	65%	Indels:	21	Gaps:	5
DB:							
QY	283 GlnProGlyAlaAlaTyrLeuTyrSerIleGlnValAsnIleValGlySerSerGlyAsp	302					
QY	849 GAGCCCTGA-----TACTGTACTCATGGGTTATGTTACCGAACATGGAAT	796					
Db	303 ---valValAspThrTyrAsnLeuAlaThrGlyValArgThrValysValAlaGly	320					
QY	795 GGGTGTGAGAGACATTGATTCATTGCGCTGGGATAAGACTTGACGTCTGGAA	736					
Db	321 SerGlnPheIleIleAsnGlyLysProPheTyrPheGlyGlyLysBisGluAsp	340					
QY	735 GACCCTTCCATCATGAGAACATCCTACTCCATGTCACATGCTGAA	676					
Db	341 ThrAlaValArgGlyLysGlyHisApprolaryMetylValIleAspPheGlnLeuMet	360					
QY	675 TATGATGTCAGAGAAAGGACTAACTGGTCACTATGTAACAGATTAATCTGTT	616					
Db	361 LysTrpIleGlyAlaAsnSerPheArgThrSerHsTyrProTAlaGluGluValMet	380					
QY	615 AAGTGCCTGGTGTCTACTCTTCGCCACCGCCATATCCTATGAGAAGAAATCATG	556					
Db	381 AspPheAlaAspArgAsnGlyIleAlaValIleAspPheGluThrProAlaValGlyLeuAsn	400					
QY	555 GACCTTGTTGATAATATGGCATTTGGTATGATGAAATGCCCTGGAGCTGGTTAA	496					
Db	401 IleAlaLeuWetGlyValSerGluArgGlyAlaProGlnThrPheThrProAspIle	420					
QY	495 TAC-----CCGAAAGTTGGAACCAATCTTA	466					
Db	421 AsnAspPheThrGlnGluAlaHisGlyGlnAlaIleAspArgGluLeuIleAlaArgAsp	440					
QY	465 AACAC-----CATTAATGTTAGGAGCTGGCCACGCGATATCCTATGAGAAGAAATCATG	421					
Db	441 AsnHsIaLaserValValMetTrpPheIleAlaAngIleUroAlaSerHsIgGluAspGly	460					
QY	420 AACCGCCCTTCGTTCTGTCATGGGCTGTCGCCAATGAAACAGCCTCCAGCTCCGTG	361					
Db	461 AlaArgGluTyrPheGluProLeuThrAsnLeuThrArgGlnLeuAspProThrArgPro	480					
QY	360 GCTGCGTATTTAAACCGTGATGGTGTACACTAACGCACTTGACCTAACCCACCGGACA	301					
Db	481 IleTrpPheAlaAsnValGlyIleThrAlaThrTyrGlnLeuAspArgIleSerAspIlePhe	500					
QY	300 GTGAAAT-----GTTCCCAATGCTAACTATGACATGACGATGACCAAGGTGGACCCATG	247					
Db	501 AspValSerCysIleAsnGlyTyrPheGlyIlePheSerGlnThrGlyAspLeuIleGlu	520					
QY	246 GATGTTAATGTTGTTGAACTGTTACTTTCTGTTACATGATGCCGGACCTGGAGTT	187					
Db	521 AlaGluAlaAlaLeuGluAspLeuIleHisGlyIlePheHisArgProle	540					
QY	186 ATCCAACTCCAACTCATGATGTCAGTTGACAATGCTGAACTGCTATGAAAGCTATG	127					
Db	541 ValMetThrGluGlyGlyAlaAspThrLeuAlaGlyYeuIleSerIleLeuGlyIlePro	560					
QY	126 ATACAGAGTTGAAATGGAGCAGATTCAGGTTCACTGACCTTACCTAATG	67					
Db	561 TrpSerGluGluPheIleInvalGlnMetLeuAspMetTyrHis	574					
QY	66 TTCACTGAGAAATACCGAGAGTTGTTAGAACTACCAT	25					
RESULT 12							
CL679241	C1679241 811 bp DNA linear GSS 09-JUL-2004						
DEFINITION							
PRI0125C_C10_2 - PRI0125C (811) Mixed stage fosmid library of P. pacificus var. California. Pristionchus pacificus genomic, genomic survey sequence.							
ACCESSION	CL679241						
VERSION	CL679241.1 GI:50185841						
KEYWORDS							
GSS; Pristionchus pacificus; Nematoda; Chromadorea; Diplogasterida; Neddiplogasteridae; Pristionchus							
REFERENCE							
1 (bases 1 to 811)							
AUTHORS							
Srinivasan,J., Otto,G.W., Kahlow,U., Geissler,R. and Sommer,R.J.							
JOURNAL							
APDBdb, an AceDB database for the nematode satellite organism Pristionchus pacificus							
NUCLEIC ACIDS RES.							
32 (1), D421-D422 (2004)							
COMMENT							
Contact: Sommer RJ							
Evolutionary Biology Max-Planck-Institute for Developmental Biology							
Seemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497011601371							
Fax: 00497011601498 Email: ralf.sommer@tuebingen.mpg.de							
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.							
Seq primer: T7, CL679241 D72076, Germany							
FEATURES							
source							
Location/Qualifiers							
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/mol_type="genomic DNA" /strain="California" /db_xref="taxon:4126" /clone_id="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEPifos-5 Fosmid vector"							
ORIGIN							
Alignment Scores:							
pred. No.: 6.558-69 length: 811							
Score: 712.50 matches: 140							
Percent Similarity: 67.51% conservative: 47							
Best Local Similarity: 50.54% Mismatches: 81							
Query Match: 21.24% Indels: 9 Gaps: 5							
US-10-757-093-4 (1-634) x CL679241 (1-811)							
QY	97 IleHisAspIleValGlyTyrValArgGlyValProGlyTyr	116					
Db	1 ATTCTGAAATTTATGTTGGCAACGGCTCGTGTACAGCCGAACTTTATACGGAAAGCTTGG	60					
QY	117 SerGlnGluArgTyrLeuValArgAlaGluSerAlaThrIleGlyArgLeuTyrVal	136					
Db	61 GCAGCCAGGGCTATCTGCTCTGGTCTGATCGCCGATCTGACCGAAAGTGGTC	120					
QY	137 AsnAsnArgLeuValAlaGluIleValGlyIleValProLeuGluAspValThr	156					
Db	121 ATAAATCAGGAGTGTGAGCATCGGGGGCTATACGCCATTGAGCCGATCTCAG	180					
QY	157 GluLeuValAlaProGlyGluIleValProGlyLeuIleValAsnGluLeuThr	176					
Db	181 CGCTATGTTATGCGGGAAAGCTGACGTTACGGCTGTCGACAGCAAGCTGAC	240					
QY	177 HisGluIleProProGlyIleSerIleLeuValGlyAspArgIleGlyAsnGlyIle	196					
Db	241 TGGCACTATCCGCGGGGGATGGTACCC--GACAAGGGCAGAAAGCAG	297					
QY	197 ThrTyrGlnGlnHisIleGlnAspIleIleValValThrAspValAspGly-----Asp	234					
Db	358 ACGCCGAAACCTGGTGGAGGATTCACGGTGGGACATGCGCAGCGCTAAC	417					
QY	298 TCTTACTTCCTGATGTTAACATGCGGGGTCATCGCAGCTGAACTCAC	357					
Db	217 ValProGlnGlnHisIleGlnAspIleIleValValThrAspValAspGly-----Asp	234					
QY	358 ACGCCGAAACCTGGTGGAGGATTCACGGTGGGACATGCGCAGCGCTAAC	417					
QY	235 AsnGlyIleIleAsnTyrGlnIleValAlaAsnGlnIleThrGlyIleGlnIle	254					
Db	418 CACGGCTCTGTTGACTGGCGGTG---GTCGCCAT-----GGTGTGTCAGCGT	465					

Db	406	GACTCTTACTCTCCCGTGGGATTCCGACCGGGGCCCTCAGAGGCCAGTCCTC
QY	325	IleasnglylysproheptyrPhehrglypheglylystisGluaspThrAlaValarg
Db	466	ATCACGGAAACCTTCTATTCATGGGTCAACAAACATGAAGATGCCATATCGA
QY	345	GlyysGlyLysAspProLysThrMetValHisAspPheGlnLeuMetLysTrpIleGly
Db	526	526 GGGAGGGCTTTGACTGGCGCTGCTGGTGAAGGAGCTCACTCTGGCTGGCG 585
QY	365	AlaAsnSerPheArgThrSerHisTyroTyralGluGluValMetAspPheAlaASP
Db	586	586 GCCATGGCTTCCGACCGCCATCACCTACGGAGGAGGAGGATGCACTCTGGAC 645
QY	385	ArganglylylValleAspGluThrProAlaValGlyLeuasnileAlaLeuMet
Db	646	646 CGCTTATGGGATCCTGCGTCAATGACCAAGAGGCCTGTGTGGCCATCATGCTGTC----- 699
QY	405	GlyValSerIluSerGlyLalaProGlnThrPheThrProAspAlaIleAsnAspThr
Db	700	700 ----- -CAGACTACGACRATGTC 720
QY	425	GlnGluAlaLysLysGlnAlaLysLysGluLysLeuAlaLysGlyPheBashBalaSer
Db	721	721 CTGCGACCACTCTGGAGGTGATGGGGAGCTGGCTGGCTGGATGAACTCACCTCT 780
QY	445	valValMetTyrSerIleAlaAsnGluProLysAspHisGluAspIleAlaArgGlyThr
Db	781	781 GTAGTCATGFGTCTGTAAGCCAAATGAGCCACTTCTCTCTGAAAGCCTGCTCTACTAC 840
QY	465	PheGluIluProLeuIleAsnIluThrArgGlnIle
Db	841	841 TTCAAGACGCTGATGCTCACACGAGGCCCT 873